

GenCore version 5.1.6
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M nucleic - nucleic search, using sw model

run on: October 6, 2003, 09:43:17 ; Search time 4541 Seconds
(without alignments)
16207.095 Million cell updates/sec

title: us-10-092-063-2

effect score: 1799

sequence: 1 ggggggtgcgcgaagggt.....cgacgcttcacagtgcca :799

scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

searched:

2888711 seqs, 2045481385 residues

total number of hits satisfying chosen parameters: 5777422

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase :

GenEmbl:

1: gb_ba:

2: gb_hg:

3: gb_in:

4: gb_cm:

5: gb_ov:

6: gb_pat:

7: gb_ph:

8: gb_pi:

9: gb_pr:

10: gb_ro:

11: gb_sts:

12: gb_sy:

13: gb_uni:

14: gb_vi:

15: em_ba:

16: em_fun:

17: em_hum:

18: em_in:

19: em_mu:

20: em_om:

21: em_or:

22: em_ov:

23: em_pat:

24: em_ph:

25: em_pi:

26: em_ro:

27: em_sts:

28: em_un:

29: em_vi:

30: em_htg_hum:

31: em_htg_inv:

32: em_htg_other:

33: em_htg_mus:

34: em_htg_pln:

35: em_htg_rdd:

36: em_htg_mam:

37: em_htg_vrt:

38: em_sy:

39: em_htgo_hum:

40: em_htgo_mus:

41: em_ntgo_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1794.8	99.8	1799	6	AR181064	AR181064 Sequence
2	1794.8	99.8	1799	6	AR210057	AR210057 Sequence
3	1794.8	99.8	1799	6	AR227867	AR227867 Sequence
4	1794.8	99.8	1799	6	AR244596	AR244596 Sequence
5	1575	87.5	1998	6	AR194794	AR194794 Sequence
6	1575	87.5	1998	9	AF039918	AF039918 Homo sapi
7	1504.2	83.6	2033	9	AF136572	AF136572 Homo sapi
8	1445	80.3	1601	6	AR181083	AR181083 Sequence
9	1445	80.3	1601	6	AR227886	AR227886 Sequence
10	1445	80.3	1601	6	AR244615	AR244615 Sequence
11	1287	71.5	1287	6	AR181065	AR181065 Sequence
12	1287	71.5	1287	6	AR210059	AR210059 Sequence
13	1287	71.5	1287	6	AR227868	AR227868 Sequence
14	1287	71.5	1287	6	AR244597	AR244597 Sequence
15	1286.4	71.5	1157	9	BC020966	BC020966 Homo sapi
16	1277.4	71.0	1287	6	AR181066	AR181066 Sequence
17	1277.4	71.0	1287	6	AR210059	AR210059 Sequence
18	1277.4	71.0	1287	6	AR227869	AR227869 Sequence
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21	1081.2	60.1	1750	10	AF084569	AF084569 Mesocrice
22	1073	59.6	1633	10	MMU238636	MMU238636 Mus muscu
23	1070.8	59.5	1749	10	AF084568	AF084568 Mesocrice
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30	342.2	13.0	2762	6	AR181084	AR181084 Sequence
31	342.2	13.0	2762	6	AR181107	AR181107 Sequence
32	342.2	13.0	2762	6	AR194792	AR194792 Sequence
33	342.2	13.0	2762	6	AR227887	AR227887 Sequence
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38	340.6	18.9	2693	6	AX591674	AX591674 Sequence
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42	339	18.8	2564	9	AK074691	AK074691 Homo sapi
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44	331.8	18.4	2458	10	RNO27748	AJ277748 Rattus no
45	320.6	17.8	2371	6	AR181101	AR181101 Sequence

ALIGNMENTS

RESULT 1	AR181064	Sequence 2 from patent US 6335013.	1799 bp	DNA	linear	PAT 20-APR-2002
LOCUS	AR181064	Sequence 2 from patent US 6335013.				
DEFINITION	AR181064					
ACCESSION	AR181064					
VERSION	AR181064.1	GI:20223278				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1799)					
AUTHORS	Ford, J., Mulero, J. J. and Yeung, G.					
TITLE	Methods and materials relating to CD39-like polypeptides					
JOURNAL	Patent: US 6335013-A 2 01-JAN-2002;					
FEATURES	Location/Qualifiers					

BASE COUNT		/organism="unknown"				467 a 409 c 472 g 442 t 9 others			
ORIGIN									
Query Match		99.8%; Score 1794.8; DB 6; Length 1799;							
Best Local Similarity		100.0%; Pred. No. C;							
Matches 1799; Conservative		0; Mismatches 0; Indels 0; Gaps 0;							
2y	1	GGGGCTGCGGCGCAAGGCTGCGCGCGCGGCTTTCTCTTCTCTGCTCAACAAAGAAA	60						
Db	1	GGGGCTGCGGCGCAAGGCTGCGCGCGCGGCTTTCTCTTCTCTGCTCAACAAAGAAA	60						
2y	61	TGTGGAGTGTCTTGGCTGTAATCCTCATACAGACAGATCATATTGCTGTCTTAGGTGA	120						
Db	61	TGTGGAGTGTCTTGGCTGTAATCCTCATACAGACAGATCATATTGCTGTCTTAGGTGA	120						
2y	121	AAAAGTGATATAATAAGGAACCAAGGAGAAAAATTCAGAGGAAGAAAAAATTCGCTCT	180						
Db	121	AAAAGTGATATAATAAGGAACCAAGGAGAAAAATTCAGAGGAAGAAAAAATTCGCTCT	180						
2y	181	GCAGGTGTGCGAGCAGGATTCGTTCTGCAACAAAGGCTCCACGCCACATCTTGGGA	240						
Db	181	GCAGGTGTGCGAGCAGGATTCGTTCTGCAACAAAGGCTCCACGCCACATCTTGGGA	240						
2y	241	AAAGAAATGGCACTTCTTGGGCGCAGCTCTTTTCATGCTGCTGCTATCTCTGTCTTGA	300						
Db	241	AAAGAAATGGCACTTCTTGGGCGCAGCTCTTTTCATGCTGCTGCTATCTCTGTCTTGA	300						
2y	301	GGCTGTCTCCACAGGAACAGCAGACTTGGTTTGGGGTATCTTCTGTCTTCCATGT	360						
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2y	361	GGCCCATCAATGTACGCGCCAGCAGCTTGTATGGAATTTATGTTGATGCGAGGAGACTG	420						
b	361	GGCCCATCAATGTACGCGCCAGCAGCTTGTATGGAATTTATGTTTGTGCGAGGAGACTG	420						
2y	421	GAACTCGAATTCATGTTTACACTTTGTGCAAGAAATGCCAGGACAGCTTCCAAATCTAG	480						
b	421	GAACTCGAATTCATGTTTACACTTTGTGCAAGAAATGCCAGGACAGCTTCCAAATCTAG	480						
2y	481	AGGGGAGTGTTCATCTGTGAGCCAGGACTTCTGCTTTTGTAGATCAACTTAAGC	540						
b	481	AGGGGAGTGTTCATCTGTGAGCCAGGACTTCTGCTTTTGTAGATCAACTTAAGC	540						
2y	541	AGGGTGTGAGACCGTTTCAAGGGCTCTTAGAGGTGGCCAAAGATCAATCCCCGAAATC	600						
b	541	AGGGTGTGAGACCGTTTCAAGGGCTCTTAGAGGTGGCCAAAGATCAATCCCCGAAATC	600						
2y	601	ACTGGAAGAACCCAGTGTCTTAAAGGCAACAGCAGGACTAGCTTACTGCCAGAAC	660						
b	601	ACTGGAAGAACCCAGTGTCTTAAAGGCAACAGCAGGACTAGCTTACTGCCAGAAC	660						
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2y	721	TACCAAGGGCAGTGTAGCATATGATGGATGGATCCGACAAAGGCAATATTAGCTTGGTTA	780						
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2y	901	AAACTCTAGGGGCTACCTCACTTCTCTTGTAGATGTGTTTAAAGCACTTATTAAGCTCTATA	960						
b	901	AAACTCTAGGGGCTACCTCACTTCTCTTGTAGATGTGTTTAAAGCACTTATTAAGCTCTATA	960						
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Db	961	CACATAGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTCGGGAGCCCTGG	1020						
Qy	1021	AGACAGAGGAGCTGATGGGCACACTTTCCGGAGTGCCTGTTTACCGAGATGTTGGAAG	1080						
Db	1021	AGACAGAGGAGCTGATGGGCACACTTTCCGGAGTGCCTGTTTACCGAGATGTTGGAAG	1080						
Qy	1081	CAGAGTGGATCTTTGGGGTGTGAAATACCAAGTATGTCGCAACCAAGAGAGGGAGTGG	1140						
Db	1081	CAGAGTGGATCTTTGGGGTGTGAAATACCAAGTATGTCGCAACCAAGAGAGGGAGTGG	1140						
Qy	1141	GCTTTGAGCCCTGCTATGCCGAAGTGTGAGGGTGTACAGGAAAACTTCAACAGCCAG	1200						
Db	1141	GCTTTGAGCCCTGCTATGCCGAAGTGTGAGGGTGTACAGGAAAACTTCAACAGCCAG	1200						
Qy	1201	AGGAGTCCAGAGAGTTCCTTCTATGCTTCTTCTACTATTAAGCCAGAGCTGTTGACA	1260						
Db	1201	AGGAGTCCAGAGAGTTCCTTCTATGCTTCTTCTACTATTAAGCCAGAGCTGTTGACA	1260						
Qy	1261	CAGACATGATTGATTATGAAAGGGGGTATTTTAAAGTTTGAAGATTTTGAAGAAAAAG	1320						
Db	1261	CAGACATGATTGATTATGAAAGGGGGTATTTTAAAGTTTGAAGATTTTGAAGAAAAAG	1320						
Qy	1321	CCAGGAAAGTGTGTATAAATTGGAAAACTTCACTCAGGAGTCTTCTCTGTGATGG	1380						
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Qy	1381	ATCTCAGTACATCACAGCCCTGTTTAAAGGATGGCTTTGGCTTTGCGAGAGCAGCTCT	1440						
Db	1381	ATCTCAGTACATCACAGCCCTGTTTAAAGGATGGCTTTGGCTTTGCGAGAGCAGCTCT	1440						
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Db	1441	TACAGCTCACAAGAAAGTGAACAACTAGAGAGCGGCTGGGGCTTGGGGCCACCTTTC	1500						
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Db	1501	ACCTTTGAGTCTCTGGGCATCTCCCATTTAGGCGCAGTACTTCTTGGAGACCTGCAT	1560						
Qy	1561	TTGCCAACACCTTTTAAAGGGAGAGAGAGCACTTAGTTTCTGAACTAGTCTGGGGACA	1620						
Db	1561	TTGCCAACACCTTTTAAAGGGAGAGAGAGCACTTAGTTTCTGAACTAGTCTGGGGACA	1620						
Qy	1621	TCCTGAGCTTGGAGCTTAGAGTTTAAATTAASCGCCGAGCTTATCTTWTATAGGT	1680						
Db	1621	TCCTGAGCTTGGAGCTTAGAGTTTAAATTAASCGCCGAGCTTATCTTWTATAGGT	1680						
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Qy	1741	TTGASAMATCCCTTTCGAGCTGCGATACCAAAAAGCCAGCGCTTCCACAGTGCCA	1799						
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RESULT 3
AR227867
LOCUS AR227867 1799 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 2 from patent US 6447771.
ACCESSION AR227867
VERSION AR227867.1 GI:27266475
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1799)
AUTHORS Ford, J., Mulero, J.J., and Yeung, G.
TITILE Methods and materials relating to novel CD39-like polypept.des
JOURNAL Patent: US 6447771-A 2 10-SEP-2002;
FEATURES Location/Qualifiers
1..1799
/organism="unknown"
source

BASE COUNT	467 a	409 c	472 g	442 t	9 others
ORIGIN					
Query Match	99.8%	Score 1794.8	DB 6	Length 1799	
Best Local Similarity	100.0%	Pred. No. 0			
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Db	61	TGTGGAGTGTCTGGCTGAATCTCTATCAGACAAGATCATTTATGTGCTGTAGGTGA	120		
QY	121	AAAGTGTATATATAAAGAGAACCAAGCGAGAAATTCAGAAGGAAAGAAAAATTCGCTCT	180		
Db	121	AAAGTGTATATATAAAGAGAACCAAGCGAGAAATTCAGAAGGAAAGAAAAATTCGCTCT	180		
QY	181	GCAGTGTGCGACAGAGATTGCTTCTTGCAACAAAGCCTCCACCCAGCACATCTTTGGGA	240		
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QY	241	AAAGAAATGCCACTCTCTGGGCACAGTCTTTTTCATGCTGGTGTATCCTGTGTGTGCA	300		
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QY	301	GGCTCTCTCCACAGGAACCCAGCAGACTTGGTTTGAGGTATCTTCTGTCTCCATGT	360		
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QY	361	GCSCCATCATGTCCAGGCACAGCCTCTGTACGAATATGTTTATGACGGAGGACCTG	420		
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RIGIN

Query Match 99.8%; Score 1794.8; DB 6; Length 1799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5

AR194794 1998 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 5 from patent US 6350447.
DEFINITION
ACCESSION AR194794
VERSION AR194794.1 GI:20244231
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1998)
AUTHORS Chadwick, B. Paul, and Frischauf, A.-M.
TITLE Methods and compositions relating to CD39-like polypeptides and
nucleic acids
JOURNAL Patent: US 6350447-A 5 26-FEB-2002;
FEATURES Location/Qualifiers
1..1998
/organism="unknown"
BASE COUNT 557 a 449 c 491 g 501 t

ORIGIN

Query Match 97.5%; Score 1575; DB 6; Length 1998;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1620; Conservative 2; Mismatches 2; Indels 25; Gaps 2;

24 GCGGCGGTTTCTCTGTTCTCGTCAACAAAGAAATGTGGAGTGTCTTGGCTGTAATCC 83
1 GCGGCGGTTTCTCTGTTCTCGTCAACAAAGAAATGTGGAGTGTCTTGGCTGTAATCC 60
84 TCATACACAGAGATCAATATGTTGCTCTT-----AGTTG 119
61 TCATACACAGAGATCAATATGTTGCTCTTGTAGTAGGACTTGTATCCAGATGTAAAGTTG 120
120 AAAAGTGATATAATAAGAAACCAAGAGAGAAATTCAGAAAGAAAGAAATTCGCTC 179
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241 AAAAGTAAGGCACTCTTGGGACACAGTCTTCTCATGCTGGTGTATCTCTGTTTGC 300
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781 ACTGTGANTTTCTGACAGTTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
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841 GACCTAGGGGAGCTCCACCAATACGTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
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1620 ATCTGGACTTGGAGCTAGAGATTWGGT 1648

RESULT 6
AF039918
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE

AF039918 Homo sapiens CD39L4 (CD39L4) mRNA, complete cds.
AF039918 Homo sapiens CD39L4 (CD39L4) mRNA, complete cds.
AF039918.1 GI:3335101
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1998)
Chadwick, B.P., Williamson, J., Sheer, D. and Frischauf, A.-M.
cDNA cloning and chromosomal mapping of a mouse gene with homology to NTPases
Mamm. Genome (1997) In press
2 (bases 1 to 1998)
Chadwick, B.P. and Frischauf, A.M.
The CD39-like gene family: identification of three new human members (CD39L2, CD39L3, and CD39L4), their murine homologues, and a member of the gene family from *Drosophila melanogaster*
Genomics 50 (3), 357-367 (1998)
98341119
9676430
3 (bases 1 to 1998)
Chadwick, B.P. and Frischauf, A.-M.
Direct Submission

JOURNAL	Submitted (15-DEC-1997)	MAMM, ICRF, 44 Lincoln's Inn Fields, London
	WC2A 3PX,	England, UK
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BASE COUNT	557 a 449 c 491 g 501 t	
IGIN		
Query Match	87.5%; Score 1575; DB 9; Length 1998;	
Best Local Similarity	98.2%; Pred. No. 0;	
Matches 1620; Conservative	2; Mismatches 2; Indels 25; Gaps 2;	
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1389	CACCTCAGGAGTCTTCTCTGTCATGAGTCTCAGCTACATCACAGCCCTGTTTAAAGGA	1448
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RESULT 8
 LOCUS AR181083 1601 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 24 from patent US 6335013.
 ACCESSION AR181083
 VERSION AR181083.1 GI:20223297
 KEYWORDS
 ORGANISM Unknown.
 SOURCE Unknown.
 UNCLASSIFIED.
 1 (bases 1 to 1601)
 AUTHORS Ford, J., Mulero, J.J. and Yeung, G.
 TITLE Methods and materials relating to CD39-like polypeptides
 JOURNAL Patent: US 6335013-A 24 01-JAN-2002;
 FEATURES
 Location/Qualifiers
 source 1..1601
 /organism="unknown"
 CASE COUNT 436 a 352 c 428 g 385 t
 ORIGIN

Query Match 80.3%; Score 1445; DB 6; Length 1601;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 301 GCGCTGTCTCCACAGGAACACAGCAGCTTGGTTTGGAGGTATCTTCTGTCTTCCAT 360
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 DB 841 ACCTAGGGGAGCTCCACCAATCACTTTCTGCCCCAGTTTGACAAAACCTCTGGAAC 900
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 DB 1441 TACAG 1445

RESULT 9
 LOCUS AR227886 1601 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 24 from patent US 6447771.
 ACCESSION AR227886
 VERSION AR227886.1 GI:27266494
 KEYWORDS

ORIGIN Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1601)
AUTHORS Ford J., Mulero, J.J. and Yeung G.
TITLE Methods and materials relating to novel CD39-like polypeptides
JOURNAL Patent: US 647771-A 24 10-SEP-2002;
FEATURES
Location/Qualifiers
1..1601
source /organism="unknown"
BASE COUNT 436 a 352 c 428 g 385 t
REGION
Query Match 80.3%; Score 1445; DB 6; Length 1601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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b 61 TGTGGAGTGTCTTGGGTGAATCTCATACAGCAAGATCATATGCTGTGTTAGTTGA 120
y 121 AAAAGTCATATATAAGGAACCAAGGAGGAGAAATTCAGAGGAGAAAGAAATTCGCTCT 180
b 121 AAAAGTCATATATAAGGAACCAAGGAGGAGAAATTCAGAGGAGAAAGAAATTCGCTCT 180
y 181 GCAGGTGTGGAGCAGGATGTCTTCTGCAACAAAGCCCTCCAGCCAGCATCTTGGGA 240
b 181 GCAGGTGTGGAGCAGGATGTCTTCTGCAACAAAGCCCTCCAGCCAGCATCTTGGGA 240
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DB 1441 TACAG 1445
RESULT 10.
AR244615
LOCUS Sequence 24 from patent US 6476211.
DEFINITION AR244615
ACCESSION AR244615
VERSION AR244615.1 GI:27292480
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1601)
AUTHORS Ford J., Mulero, J.J. and Yeung G.
TITLE Methods and materials relating to CD39-like polypeptides
JOURNAL Patent: US 6476211-A 24 05-NOV-2002;
FEATURES
Location/Qualifiers
1..1601
source /organism="unknown"
BASE COUNT 436 a 352 c 428 g 385 t
ORIGIN
Query Match 80.3%; Score 1445; DB 6; Length 1601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GCGGGTGGCGCCCAAGGTTGGCGCGCGCGTTTCCTTGTCTCTGGTCAACAAGAAA 60

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301 GCGCTCTCCACAGAACCCAGCAGCTTGTGAGGGTATCTCTGCTCTCCATGT 360
b GCGCTCTCCACAGAACCCAGCAGCTTGTGAGGGTATCTCTGCTCTCCATGT 360
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RESULT 11
AR181065
LOCUS AR181065 1287 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 4 from patent US 6335013.
ACCESSION AR181065
VERSION AR181065.1 GI:20223279
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1287)
AUTHORS Ford, J., Mulero, J. J. and Yeung, G.
TITLE Methods and materials relating to CD39-like polypeptides
JOURNAL Patent: US 6335013-A 4 01-JAN-2002;
FEATURES
Location/Qualifiers
1..1287
source
BASE COUNT 330 a 290 c 344 g 323 t
ORIGIN

Query Match 71.5%; Score 1287; DB 6; Length 1287;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 546 GCTGAGACCGTTCAGAGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGG 605
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Query Match	Best Local Similarity	Matches 1287	71.5%	Score 1287	DB 6	Length 1287	Indels	Gaps
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146	GAGCCCTGCTATGCGAAGTGGCTGAGGGTGGTACGAGGAAAACTTCACCAAGCCAGAGGAG	1205						
901	GAGCCCTGCTATGCGAAGTGGCTGAGGGTGGTACGAGGAAAACTTCACCAAGCCAGAGGAG	960						
1206	GTCAGAGAGGTTCTCTTCTATGCTTTTCTTTACTATTATGACGAGGCTGTGTACACAGAC	1265						
961	GTCAGAGAGGTTCTCTTCTATGCTTTTCTTTACTATTATGACGAGGCTGTGTACACAGAC	1020						
1266	ATGATTTGATTATGAAGAGGGGGGTATTTTAAAGTTTGAGGATTTTGAAGAAAGAGCCAGG	1325						
1021	ATGATTTGATTATGAAGAGGGGGGTATTTTAAAGTTTGAGGATTTTGAAGAAAGAGCCAGG	1080						
1326	GAAGTGTGTGATACTTTGGAAAACTTCACCTCAGGCAGTCTCTTTCTGTGATGGATCTC	1385						
1081	GAAGTGTGTGATACTTTGGAAAACTTCACCTCAGGCAGTCTCTTTCTGTGATGGATCTC	1140						
1386	AGCTACATACAGCCCTGTTTAAAGATGGCTTTGGCTTTGCAGACAGCAGTCTTTACAG	1445						
1141	AGCTACATACAGCCCTGTTTAAAGATGGCTTTGGCTTTGCAGACAGCAGTCTTTACAG	1200						
1446	CTCACAAGAAAGTGAACAAATAGAGAGCGGCTGGGGCTTGGGGGCCACTTTCACCTG	1505						
1201	CTCACAAGAAAGTGAACAAATAGAGAGCGGCTGGGGCTTGGGGGCCACTTTCACCTG	1260						
1506	TTGCAGTCTCTGGGCATCTCCCATTTGA	1532						
1261	TTGCAGTCTCTGGGCATCTCCCATTTGA	1287						
RESULT 13								
AR227868	Sequence 4 from patent US 644771.							
AR227868	GI:27266476							
Unknown:								
Unknown:								
Unclassified:								
1 (bases 1 to 1287)								
Ford, J., Mulero, J. J. and Yeung, G.								
Methods and materials relating to novel CD39-like polypeptides								
Patent: US 644771-A 4 10-SEP-2002;								
Location/Qualifiers								
1..1287								
/organism="unknown"								
330 a 290 c 344 g 323 t								
Query Match	71.5%	Score 1287	DB 6	Length 1287				
Best Local Similarity	100.0%	Pred. No. 0						
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D5	241	GAAGT	TTTTGATTCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACTTAAGCAGGGT	300
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D5	721	AGTTACTCTGGATTTCGATTGAAAGCTGCAAGACTAGCAACCTCGGAGCCCTGGAGACA	780	
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D5	781	GAAGGACTGATGGGCACACTTTTCCGAGTGCCCTGTTTACCGAGATGGTTTGGAGAGCAG	840	
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D5	841	TGATCTTTGGGGGTGTGAATACCACTAGTGTGGCCAAACCAAGAGGGAGTGGGGCTTT	900	
QY	1146	GAGCCCTGCTATGCCGAAGTCTCGAGGTGGTACGAGGAAACTTCACCAAGCCAGAGGAG	1205	
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D5	1201	CTCAGAAAGAAAGTGAACAACATAGAGAGGGGCTGGGCCCTTGGGGGCCACCTTTACCTG	1260	
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D5	1261	TTGAGTCTCTGGGCATCTCCCATCGA	1287	

RESULT 14
AR244597

Accession	Source	Query Match	Best Local Similarity	Matches	Score	DB	Length	Indels	Gaps
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AR244597.1	GI:27294262	Unclassified.	Unclassified.	0	1287	323	344	0	0
AR244597.1	GI:27294262	1 (bases 1 to 1287)	Conservative	0	1287	323	344	0	0
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AR244597.1	GI:27294262	1 (bases 1 to 1287)	Conservative	0	1287	323	344	0	

QY	1026	GAAGGACCTGATGGGCACACTTTCCCGAGTGCCCTGTTTACCGAGA*GGTTGGGAAGCAGAG	1081
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QY	1086	TGCGATCTTTGGGGGTGTGAATACCAAGTATGGTGGCAACCAAGAGGGAGGTGGGCTTT	1145
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QY	1146	GAGCCCTGCTATGCCGAAGTGCTGAGGGTGGTACGAGGAAAACTTCACCAAGCAGAGGAG	1205
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QY	1206	GTCGAGAGAGGTTCCCTTCTATGCTTCTCTACTATATGACCGAGCTGTTGACACAGAC	1265
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QY	1386	AGCTACATCACGCCCTGTTAAAGGATGCTTTGGGCTTTCACAGACGACAGCTTTACAG	1445
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QY	1446	CTCACAAGAAAGTGAAACAATAGAGAGCGGGCTGGGCGCTTGGGGGCCACCTTTACCTG	1505
DB	1201	CTCACAAGAAAGTGAAACAATAGAGAGCGGGCTGGGCGCTTGGGGGCCACCTTTACCTG	1360
QY	1506	TTGCAGTCTCTGGGATCTCCCATTTGA	1532
DB	1261	TTGCAGTCTCTGGGATCTCCCATTTGA	1287
RESULT 15			
BC020966			
LOCUS			
DEFINITION	Homo sapiens, Similar to ectonucleoside triphosphate di-phosphohydrolase 5, clone MGC:9127 IMAGE:3847878, mRNA, complete cds.		
ACCESSION	BC020966		
VERSION	BC020966.1		
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Strausberg,R.		
TITLE	Direct Submission		
JOURNAL	Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgapsb-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www.shgc.stanford.edu Contact: (Dickson, Mark) mcd@axil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.		
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov			

Series: IRAK Plate: 20 Row: 5 Column: 19
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4557426.
Location/Qualifiers

FEATURES

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QTPRGILTSFENFTYKDLTHSYLPGKAKRLATLGALETDGHTFRSACLPRW
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FADSTVLOHIISWN"

BASE COUNT 917 a 723 c 792 g 725 t

ALIGN

Query Match 71.5%; Score 1286.4; DB 9; Length 3157;
Best Local Similarity 91.1%; Pred. No. G; Mismatches 1; Indels 141; Gaps 2;
Matches 1448; Conservative 0;

1 GCGGCTCGCGGCAAGGTGGCGCGCGCTTTCTTGTTCTCTGTGTCACAAAGAAA 60
|||||
12 GCGGCTCGCGGCAAGGTGGCGCGCGCTTTCTTGTTCTCTGTGTCACAAAGAAA 71
|||||

61 TGTGAGTGTCTTGCTGTAATCTCATACAGAAAGATCATTATGCTGCTT----- 113
|||||
72 TGTGAGTGTCTTGCTGTAATCTCATACAGAAAGATCATTATGCTGCTGTTAGGTAGG 131
|||||

114 -----AGTTGAAAGATGATTAATAAGGAACCAAGGAGAAATTC 156
|||||
132 ACTTGATATCCAGATGTAAGTTTGAAGAGTGAATAATAAGGAACCAAGGAGAAATTC 191
|||||

157 AGAAGAAAGAAAGAAATTT----- 174
|||||
192 AGAAGAAAGAAAGAAATTTGCTCTACTCTGTCACCGAGGCTGGAGTACAGTGGTSCAATC 251
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175 ----- 174
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252 ACAGCTCACGGCAGCTTCAAACTCTGGGCTCAAGCGATCCTCTGCTCAACCTTCCCGA 311
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175 -----GCTCTCAGGTGTCGAGGAGGATGCTTCTGCAACAAAGGCT 219
|||||

312 GTAGCTGAGCTACAGCTCTCGAGGTGTCGAGGAGGATGCTTCTGCAACAAAGGCT 371
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220 CCACCCAGCCACATCTTGGGAAAGAAATGGCCACTCTTGGGGCACAGTCTTTTTCATGC 279
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372 CNACCCAGCCACATCTTGGGAAAGAAATGGCCACTCTTGGGGCACAGTCTTTTTCATGC 431
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280 TGTGTGATCTCTGTGTTGTCAGGCTGTCTCCACAGGAACCAAGGAGCTTGGTTGAGG 339
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340 GTATCTTCTGCTCTCCATGTGCCCCCATCAATGTAGGCCAGGACCTTGATGGAATTA 399
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400 TGTGTTGATCGAGGAGCACTTGAACCTCGAATTCATGTTTACACCTTTGTCAGGAATTCGC 459
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Job time : 4548.secs

GenCore version 5.1.6
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4 nucleic - nucleic search, using sw model

run on: October 6, 2003, 09:40:42 ; Search time 377 Seconds
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12881.403 Million cell updates/sec

File: US-10-092-063-2

Effect score: 1799

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Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	1794.8	99.8	1799	21	AA250356 Human CD39-L4 prot
2	1794.8	99.8	1799	22	AA250356 Human CDNA encodin
3	1575	87.5	1998	21	AA250356 Human ecto-phospha
4	1575	87.5	1998	24	AA250356 Human CD39-L4 cDNA.
5	1445	80.3	1601	21	AA250356 Human CD39-L46 pro
6	1445	80.3	1601	21	AA250356 Human cDNA encodin
7	1287	71.5	1287	22	AA250356 Human CD39 like pr
8	1277.4	71.0	1287	21	AA250356 Human CD39-L4 vari

9	1277.4	71.0	1297	22	AAF63385	DNA encoding human
10	1089.2	60.5	1457	21	AA250356	Human colon cancer
11	1049.6	58.3	2119	24	AA250356	Mouse CD39-L4 cDNA
12	415.2	23.1	799	22	AA250356	Human breast cancer
13	363.4	20.2	488	23	ABV43087	Human prostate exp
14	363.2	20.2	480	23	ABV22557	Human prostate exp
15	363.2	20.2	480	23	ABV28387	Human prostate exp
16	359.2	20.0	420	25	ABX46587	Bovine EST associat
17	359.2	20.0	798	22	AA250356	Human breast cancer
18	342.2	19.0	2693	22	AA250356	Human CT39-L2 spli
19	342.2	19.0	2762	21	AA250356	Human ecto-phospha
20	342.2	19.0	2762	22	AA250356	Human CD39-L2 codi
21	342.2	19.0	2762	22	AA250356	Human CD39-L2 spli
22	342.2	19.0	2762	24	AA250356	Human CD39-L2 cDNA
23	340.6	18.9	2693	24	ABT05470	DNA of NCVX 15a SE
24	340.6	18.9	2736	24	ABU39778	Human NS cDNA sequ
25	339	18.8	2564	22	AA250356	Human full-length
26	339	18.8	2648	24	ABT05471	DNA of NCVX 15b SE
27	332.6	18.5	455	23	ABV13105	Human prostate exp
28	330.8	17.8	475	23	ABV34226	Human prostate exp
29	330.6	17.8	2371	22	AA250356	Human CD39-L2 spli
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31	320	17.8	342	24	ABV88403	Human colon cancer
32	303.6	16.9	9365	21	AA250356	Human CD39-L4 geno
33	303.6	16.9	9365	22	AA250356	Human CD39 like pr
34	300.6	16.7	458	22	AA250356	Human breast cancer
35	300	16.7	300	21	AA250356	EST to isolate hum
36	300	16.7	300	22	AA250356	Human cDNA used to
37	296.6	16.5	2294	22	AA250356	Human CD39-L2 spli
38	294.6	16.4	855	22	AA250356	Human breast cancer
39	290.8	16.2	1498	22	AA250356	DNA encoding matu
40	290.8	16.2	2805	22	AA250356	Human CD39-L2 spli
41	290.2	16.1	1002	22	AA250356	Human immune/haema
42	290.2	16.1	14747	22	AA250356	Human CD39 like pr
43	290.2	16.1	15977	22	AA250356	Human CD39 like pr
44	284.6	15.8	442	22	AA250356	Human breast cancer
45	282.4	15.7	404	23	ABV03936	Human prostate exp

ALIGNMENTS

RESULT :
AA250356
ID AA250356 standard; cDNA; 1799 BP.
AC AA250356;
XX
XX 18-MAY-2000 (first entry)
XX Human CD39-L4 protein encoding cDNA.
XX
XX CD39-L4; human; apyrase; nucleotide diphosphatase; NDPase;
ATP diphosphohydrolase; ATPase; adenosine diphosphate; ADP; treatment;
platelet aggregation; antithrombotic; thrombosis; myocardial infarction;
cerebral ischaemia; angina; vascular graft; extracorporeal circulation;
molecular weight marker; nutritional supplement; tumour; prevention;
drug targeting; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
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FT /note= "Homologous to the CD39 family"
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FT /note= "Comprises hydrophobic stretch of amino acids"
FT mat_peptide 312..1529
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FT /note= "Homologous to human and murine CD39"

	CC	with venous thrombosis. CD39-14 and CD39-12 polypeptides are useful in
	CC	modulating disease states (including platelet aggregation, inflammation
	CC	and apoptosis) associated with ADP or other purinergic signalling by
	CC	reducing the levels of NDPs. The polypeptides are also useful for
	CC	prophylaxis or treatment of inflammation related disorders, such as
	CC	disorders involving sepsis or systemic inflammatory response syndrome or
	CC	SIRS (and associated conditions) such as fever, tachycardia, tachypnea,
	CC	cytokine overstimulation; autoimmune disorders such as thrombopneia,
	CC	atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,
	CC	cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis;
	CC	neurological disorders including neurodegenerative diseases, epilepsy,
	CC	depression, Alzheimer's disease, Parkinson's disease, Huntington's
	CC	disease, and amyotrophic lateral sclerosis; and cancer. The present
	CC	sequence represents cDNA encoding CD39 like protein CD39-14.
XX		
SQ		Sequence 1799 BP; 467 A; 409 C; 472 G; 442 T; 9 other;
		Query Match 99.8%; Score 1794.8; DB 22; Length 1799;
		Best Local Similarity 100.0%; Pred No. 0;
		Matches 1799; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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Dd	1	GCGGGCTGCGCGCAAGGGTGGCGGCGCGGTTCCTTTCTTGTCGAACAAAGAAA 6D
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Qy	721	TACCAAAGGGCAGTTAGCATCATGATGCATCCGACGAAGACGCAATTATGCTTGGGTTA 780
Dd	721	TACCAAAGGGCAGTTAGCATCATGATGCATCCGACGAAGACATATTATCTTGGGTTA 780

360 TGCCCCATCAATGTCAGGCCAGCACCTTGTATGGAATTATGTTGATCGAGGAGCACT 419
361 TGCCCCATCAATGTCAGGCCAGCACCTTGTATGGAATTATGTTGATCGAGGAGCACT 420
420 GGAATCGAATTATGTTTACACCTTTGTCAGAAAATGCCAGGACAGCTTCAATTTCTA 479
421 GGAATCGAATTATGTTTACACCTTTGTCAGAAAATGCCAGGACAGCTTCAATTTCTA 480
480 GAAGGGAGGTTTTCATCTGTGAAGCCAGGACTTCTGCTTTGTATGATCAACCTTAG 539
481 GAAGGGAGGTTTTCATCTGTGAAGCCAGGACTTCTGCTTTGTATGATCAACCTTAG 540
540 CAGGGTCTGAGACCCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCGCCGAAGT 599
541 CAGGGTCTGAGACCCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCGCCGAAGT 600
600 CACTGGAAGAACCCAGTGGTCTTAAGGCAACAGCAGGACTAGCTTACTGCGAGAA 659
601 CACTGGAAGAACCCAGTGGTCTTAAGGCAACAGCAGGACTAGCTTACTGCGAGAA 660
660 CACAAGCCAGGCTCTGCTCTTTGAGGTAAAGAGATCTTCAGGAAGTCACTTTCCTG 719
661 CACAAGCCAGGCTCTGCTCTTTGAGGTAAAGAGATCTTCAGGAAGTCACTTTCCTG 720
720 GTACCAAGGGCAGTGTAGCATCTGGATGATGATGATGATGATGATGATGATGATG 779
721 GTACCAAGGGCAGTGTAGCATCTGGATGATGATGATGATGATGATGATGATGATG 780
780 ACTGTGAAATTTCTGACAGTCACTGCTGATGCTGATGCTGATGCTGATGCTGATG 839
781 ACTGTGAAATTTCTGACAGTCACTGCTGATGCTGATGCTGATGCTGATGCTGATG 840
840 GACCTAGGGGAGGCTCCACCCAAATCACCTTCTGCTGCTGCTGCTGCTGCTGCTG 899
841 GACCTAGGGGAGGCTCCACCCAAATCACCTTCTGCTGCTGCTGCTGCTGCTGCTG 900
900 CAAATCTCTAGGGCTACCTCACTTCTGATGATGATGATGATGATGATGATGATG 959
901 CAAATCTCTAGGGCTACCTCACTTCTGATGATGATGATGATGATGATGATGATG 960
960 ACATAGTCTAGCTGGGATTTGGATGAAAGCTGCAAGCTAGCAACCTCGGAGCCCTG 1019
961 ACATAGTCTAGCTGGGATTTGGATGAAAGCTGCAAGCTAGCAACCTCGGAGCCCTG 1020
1020 GAGACAGAAGGACTGATGGGACACTTTCGGAGTGCCTTTTACCGAGATGGTTGGAA 1079
1021 GAGACAGAAGGACTGATGGGACACTTTCGGAGTGCCTTTTACCGAGATGGTTGGAA 1080
1080 GCAGAGTGGATCTTTGGGGGTGTAATACAGTATGTTGGTGGCAACCAAGAGGGAGGTG 1139
1091 GCAGAGTGGATCTTTGGGGGTGTAATACAGTATGTTGGTGGCAACCAAGAGGGAGGTG 1140
1140 GGCTTTGAGCCCTCTATGCGGAGTGCCTGAGGAGTGTACGAGGAAAACCTTCACCA 1199
1141 GGCTTTGAGCCCTCTATGCGGAGTGCCTGAGGAGTGTACGAGGAAAACCTTCACCA 1200
1200 GAGGAGTCCAGAGGTTCTTCTAAGCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCT 1259
1201 GAGGAGTCCAGAGGTTCTTCTAAGCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCT 1260
1260 ACACACATGATGATTAAGAGGGGGGTATTTAAAGCTTCAGACTTTTGAAGAAA 1319
1261 ACACACATGATGATTAAGAGGGGGGTATTTAAAGCTTCAGACTTTTGAAGAAA 1320
1320 GCCAGGGAAGTGTGTAATCTGAAACCTTCACCTCAGGCAAGTCTTCTCTGTCATG 1379
1321 GCCAGGGAAGTGTGTAATCTGAAACCTTCACCTCAGGCAAGTCTTCTCTGTCATG 1380
1380 GATCTCAGCTACATCAGACCCCTTTAAAGATGGCTTTTGGCTTTGAGACACACAGTC 1439
1381 GATCTCAGCTACATCAGACCCCTTTAAAGATGGCTTTTGGCTTTGAGACACACAGTC 1440
1440 TTACAGCTCAAAAGAAAGTGAACAAATAGACAGCGGCTTGGGCGCTTGGGCGCCACTT 1499

1441 TTACAGCTCAAAAGAAAGTGAACAAATAGACAGCGGCTTGGGCGCTTGGGCGCCACTT 1500
1500 CACCTGTTCAGTCTCTGGCATCTCCCATTTGAGGCAAGTACTTCTTGGAGACCTGCA 1559
1501 CACCTGTTCAGTCTCTGGCATCTCCCATTTGAGGCAAGTACTTCTTGGAGACCTGCA 1560
1560 TTTGCCAAACCTTTTAAAGGGAGGAGAGACACTTAGTTTCTGAACCTAGTCTGGGAC 1619
1561 TTTGCCAAACCTTTTAAAGGGAGGAGAGACACTTAGTTTCTGAACCTAGTCTGGGAC 1619
1620 ATCTGAGCTTGAAGCTTAGAGATTAGGT 1648
1620 ATCTGAGCTTGAAGCTTAGAGATTAGGT 1648

RESULT 4
AAD31695
ID AAD31695 standard; cDNA; 1998 BP.
XX
AC AAD31695;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human CD39L4 cDNA.
XX
KW Human; CD-39-like protein; CD39L4 protein; therapy; immune deficiency;
KW autoimmune disorder; multiple sclerosis; systemic lupus erythematosus;
KW rheumatoid arthritis; autoimmune thyroiditis; allergic reaction; asthma;
KW insulin dependent diabetes mellitus; periodontal disease; osteoporosis;
KW osteoarthritis; wound healing; tissue repair; Alzheimer's disease; ulcer;
KW Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease;
KW nervous system disease; nerve injury; ischaemia-reperfusion injury;
KW endotoxin lethality; arthritis; nephritis; inflammatory bowel disease;
KW Crohn's disease; viricide; antibacterial; antifungal; neuroprotective;
KW dermatological; immunosuppressive; vulnery; nootropic; anticonvulsant;
KW antiinflammatory; nephrotropic; gastrointestinal; vasotropic;
KW chromosome 14q24; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 247..1533
FT /*tag= a
FT /product= "Human CD39L4 protein"
XX
PN US6350447-B1.
XX
PD 26-FEB-2002.
XX
PF 29-JAN-1999; 99US-0240639.
XX
PR 29-JAN-1999; 99US-0240639.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Chadwick BP, Frischauf A;
XX
DR WP1; 2302-215262/27.
DR P-PSDB; AAE19883.
XX
PT An isolated polypeptide with phosphohydrolase activity, designated
PT CD39L2, useful to identify other proteins with which binding occurs or
PT identify inhibitors and for treatment of, e.g., Alzheimer's, multiple
PT sclerosis and osteoporosis
XX
PS Example; Fig 7; 10pp; English.
XX
CC The present invention relates to novel proteins with phosphohydrolase
CC activity, designated CD-39-like (CD39L) proteins and polynucleotides
CC encoding such proteins. CD39L proteins are useful to treat infectious
CC diseases caused by viral, bacterial, fungal or other infection that may
CC be treatable with CD39L. They are useful in the treatment of various

C immune deficiencies and disorders, autoimmune disorders such as multiple
C sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune
C thyroiditis and insulin dependent diabetes mellitus, allergic reactions
C and conditions such as asthma and other respiratory problems, periodontal
C disease, osteoporosis, osteoarthritis and other tooth repair processes.
C They may have utility in compositions used for bone, cartilage, tendon,
C ligament and/or nerve tissue growth or regeneration as well as for wound
C healing and tissue repair and replacement and in the treatment of burns,
C incisions and ulcers. CD39L proteins may also be useful for proliferation
C of neural cells and for regeneration of nerve and brain tissue, i.e. for
C the treatment of central nervous system diseases such as Alzheimer's
C disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's
C disease, peripheral nervous system diseases peripheral nerve injuries,
C peripheral neuropathy and localised neuropathies. They are also used to
C treat mechanical and traumatic disorders which involve degeneration,
C death or trauma to neural cells or nerve tissue. CD39L proteins of the
C invention are also useful to promote better or faster closure of non-
C healing wounds, including pressure ulcers, ulcers associated with
C vascular insufficiency and surgical and traumatic wounds. They also
C exhibit anti-inflammatory activity and may be used to treat inflammatory
C conditions including chronic or acute conditions, including ischaemia-
C reperfusion injury, endotoxin lethality, arthritis, nephritis, cytochrome
C or chemokine-induced lung injury, inflammatory bowel disease or Crohn's
C disease. The present sequence is human CD39L4 DNA. CD39L4 gene is
C localised on chromosome 14q24.

Sequence 1998 BP; 557 A; 449 C; 491 G; 501 T; 0 other;

Query Match 87.5%; Score 1575; DB 24; Length 1998;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1620; Conservative 2; Mismatches 2; Indels 25; Gaps 2;
Y 24 GCGGCGCGTTTCCCTGTTCTCGTCAAGAAATGAGTGGAGTGTCTGGTGAATCC 83
b 1 GCGGCGCGTTTCCCTGTTCTCGTCAAGAAATGAGTGGAGTGTCTGGTGAATCC 60
Y 84 TCATACAGACAAGATCATATGTTGGTGTGT-----AGGTTG 119
b 61 TCATACAGACAAGATCATATGTTGGTGTGTAGTAGAGCTGTATCCAGATGTAAGTTG 120
Y 120 AAAAAAGTATATAAAGGAAACCAAGGAGAAATTCAGAGGAAAGAAAAATTCGCTC 179
b 121 AAAAAAGTATATAAAGGAAACCAAGGAGAAATTCAGAGGAAAGAAAAATTCGCTC 180
Y 180 TGCAGGTGTCGAGCAGGATGCTTCTGCAACAAGACCTCCACCCAGCCACATCTTGG 239
b 181 TGCAGGTGTCGAGCAGGATGCTTCTGCAACAAGACCTCCACCCAGCCACATCTTGG 240
Y 240 AAAAAAGTATATAAAGGAAACCAAGGAGAAATTCAGAGGAAAGAAAAATTCGCTC 299
b 241 AAAAAAGTATATAAAGGAAACCAAGGAGAAATTCAGAGGAAAGAAAAATTCGCTC 300
Y 300 AGCGTGTCTCCACAGGAAACCAAGGAGAAATTCAGAGGAAAGAAAAATTCGCTC 359
b 301 AGCGTGTCTCCACAGGAAACCAAGGAGAAATTCAGAGGAAAGAAAAATTCGCTC 360
Y 360 TGCAGGTGTCGAGCAGGATGCTTCTGCAACAAGACCTCCACCCAGCCACATCTTGG 419
b 361 TGCAGGTGTCGAGCAGGATGCTTCTGCAACAAGACCTCCACCCAGCCACATCTTGG 420
Y 420 GGAATCTGAATTCATGTTTACACCTTTGTGCAAGAAATGCCAGGAGCTTCCAAATCTA 479
b 421 GGAATCTGAATTCATGTTTACACCTTTGTGCAAGAAATGCCAGGAGCTTCCAAATCTA 480
Y 480 GAAGGGAAGTTTGTATCTGTGAGCCAGGACTTCTGCTTTTGTAGATCAACTAAG 539
b 481 GAAGGGAAGTTTGTATCTGTGAGCCAGGACTTCTGCTTTTGTAGATCAACTAAG 540
Y 540 CAGGTCCTGAGCCGTTCAAGGGCTCTTGAAGTGGCCAAAGACTCAATCCCCCAAGT 599
b 541 CAGGTCCTGAGCCGTTCAAGGGCTCTTGAAGTGGCCAAAGACTCAATCCCCCAAGT 600
Y 600 CACTGGAAAAAGACCCCAAGTGGTCTTAAGGCAACAGCAGGAGCTACGCTTACTGCCAGAA 659

660 CACTGGAAAAAGACCCCAAGTGGTCTTAAGGCAACAGCAGGACTACGCTTACTGCCAGAA 660
Y 660 CACAAGGCAAGGCTCTGCTCTTTGAGGTAAAGAGATCTTTCAAGAGTCACTTCTGCTG 719
b 661 CACAAGGCAAGGCTCTGCTCTTTGAGGTAAAGAGATCTTTCAAGAGTCACTTCTGCTG 720
Y 720 GTACCAAGGCAAGGCTCTGCTCTTTGAGGTAAAGAGATCTTTCAAGAGTCACTTCTG 779
b 721 GTACCAAGGCAAGGCTCTGCTCTTTGAGGTAAAGAGATCTTTCAAGAGTCACTTCTG 780
Y 780 ACTGTGAATTTCTGACAGGTCAGTGCATGCGTCCACAGAGGAGACTTGGGACCTTG 839
b 781 ACTGTGAATTTCTGACAGGTCAGTGCATGCGTCCACAGAGGAGACTTGGGACCTTG 840
Y 840 GACCTAGGGGAGGCTCTCACCAAAATCACGTTCTCTGCCAGGTTTGAGAAACCTCTGAA 899
b 841 GACCTAGGGGAGGCTCTCACCAAAATCACGTTCTCTGCCAGGTTTGAGAAACCTCTGAA 900
Y 900 CAACTCTAGGGGAGGCTCTCACCTCTCTTGAATGTTTAAACAGACTTATAAGCTCTAT 959
b 901 CAACTCTAGGGGAGGCTCTCACCTCTCTTGAATGTTTAAACAGACTTATAAGCTCTAT 960
Y 960 ACACATAGTTTACCTGGGATTTGGAATGAAAGCTGCAAGACTAGCAACCTCGGAGCCCTG 1019
b 961 ACACATAGTTTACTTGGGATTTGGAATGAAAGCTGCAAGACTAGCAACCTCGGAGCCCTG 1020
Y 1020 GAGACAGAAGGAGCTGATGGGCACACTTTCCGGAGTGCCTTTTACCGAGATGGTTGAA 1079
b 1021 GAGACAGAAGGAGCTGATGGGCACACTTTCCGGAGTGCCTTTTACCGAGATGGTTGAA 1080
Y 1080 GCAGATGGATCTTTGGGGTGTGAATATACAGTATGCTGTCGCAACCAAGAGAGGAGG 1139
b 1081 GCAGATGGATCTTTGGGGTGTGAATATACAGTATGCTGTCGCAACCAAGAGAGGAGG 1140
Y 1140 GCTTTGAGCCCTGCTATGCGCAAGTGTCTGAGGCTGTACAGGAGAAACTTCCACAGCA 1199
b 1141 GCTTTGAGCCCTGCTATGCGCAAGTGTCTGAGGCTGTACAGGAGAAACTTCCACAGCA 1200
Y 1200 GAGGAGTCCAGAGAGGTTCTCTTCTATGCTTTCTTCTTACTATTATGACCGAGCTGTGAC 1259
b 1201 GAGGAGTCCAGAGAGGTTCTCTTCTATGCTTTCTTCTTACTATTATGACCGAGCTGTGAC 1260
Y 1260 ACAGACATGATTGATTATGANAAGGGGGGTATTTAAAGTTGAGATTTTGAAGAAAA 1319
b 1261 ACAGACATGATTGATTATGANAAGGGGGGTATTTAAAGTTGAGATTTTGAAGAAAA 1320
Y 1320 GCCAGGGAAGTGTGTGATTAACCTTGGAAAACTTCACTCAGGCACTCTTCTTCTGTGATG 1379
b 1321 GCCAGGGAAGTGTGTGATTAACCTTGGAAAACTTCACTCAGGCACTCTTCTTCTGTGATG 1380
Y 1380 GATCTCAGCTACATCAGAGCCCTCTTAAAGATGCTTTGGCTTTGAGAGCAGCAGCAGTC 1439
b 1381 GATCTCAGCTACATCAGAGCCCTCTTAAAGATGCTTTGGCTTTGAGAGCAGCAGCAGTC 1440
Y 1440 TTACAGCTCACAAGAAAGTGAACAACATAGAGACGGGCTGGGCTTTGGGGGCCACCTTT 1499
b 1441 TTACAGCTCACAAGAAAGTGAACAACATAGAGACGGGCTGGGCTTTGGGGGCCACCTTT 1500
Y 1500 CACCTGTTGAGCTCTCTGGGATCTCCCATTTGAGGCCACGCTACTTCTTGGAGACCTGCA 1559
b 1501 CACCTGTTGAGCTCTCTGGGATCTCCCATTTGAGGCCACGCTACTTCTTGGAGACCTGCA 1560
Y 1560 TTTGCCAACACCTTTTAAAGGGGAGAGAGACTTAGTTTCTGAACCTAGTCTGGGGAC 1619
b 1561 TTTGCCAACACCTTTTAAAGGGGAGAGAGACTTAGTTTCTGAACCTAGTCTGGGGAC 1619
Y 1620 ATCCTGAGCTTGAAGCTTGAAGTTTMRGTT 1648
b 1620 ATCCTGAGCTTGAAGCTTGAAGTTTMRGTT 1648

AZ50358
D AAZ50358 standard; cDNA; 1601 bp.
C AAZ50358;
X
T 18-MAY-2000 (first entry)
X Human CD39-L66 protein encoding cDNA.
X CD39-L4; human; CD39-L66; apyrase; nucleotide diphosphatase; NDase;
X ATP diphosphohydrolase; ATPase; adenosine diphosphate; ADP; treatment;
X platelet aggregation; antithrombotic; thrombosis; myocardial infarction;
X cerebral ischemia; angina; vascular graft; extracorporeal circulation;
X molecular weight marker; nutritional supplement; tumour; prevention;
X drug targeting; splice variant; ss.
X Homo sapiens.
X
X Key Location/Qualifiers
X CDS 246..1463
X /tag= a
X /product= "Human CD39-L66 protein"
X /note= "Splice variant of CD39-L4 protein."
X
X WO200004041-A2.
X
X 27-JAN-2000.
X
X 16-JUL-1999; 99WO-US16180.
X
X 16-JUL-1998; 98US-0118205.
X
X 24-JUL-1998; 98US-022449.
X
X 04-FEB-1999; 99US-024444.
X
X 19-MAR-1999; 99US-027347.
X
X 09-JUL-1999; 99US-0350836.
X
X (HYSE-) HYSEQ INC.
X
X Ford J, Mulero J;
X
X WPI; 2000-182397/16.
X
X P-PSDB; AAY44851.
X
X New nucleic acid encoding human CD39-like protein, useful for treating
X and preventing thrombotic disease -
X
X Claim 8; Page 123; 125pp; English.
X
X The present sequence is a cDNA encoding the CD39-L66 protein, a splice
X variant of CD39-L4 protein. It is an apyrase and/or nucleotide
X diphosphatase (NDase), isolated from the human foetal liver-spleen cDNA
X library, b2HFLS20W. It is a soluble ATP diphosphohydrolase (ATPase) and
X is involved in the hydrolysis of adenosine diphosphate (ADP), the agonist
X that causes platelet aggregation. CD39-L4 protein has 30% and 80%
X homology to human and murine CD39. It has platelet aggregation inhibition
X and antithrombotic activity. CD39-L4 is used to treat or prevent
X thrombosis, myocardial infarction, cerebral ischaemia and angina. It is
X also used in vitro, to maintain vascular grafts or during extracorporeal
X circulation, to hydrolyse NPP, as molecular weight markers and as
X nutritional supplements. It is used to identify therapeutic agents that
X bind and modulate CD39-L4. It is coupled to toxins for targeting drugs
X to tumours or other cells that express CD39-L4.
X
X Sequence 1601 BP; 436 A; 352 C; 428 G; 385 T; 0 other;
X
X Query Match 80.3%; Score 1445; DB 21; Length 1603;
X Best Local Similarity 100.0%; Pred. No. 0;
X Matches 1445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
X
X 1 GCGGGTGGCGGCAAGGTTGGCGCGCGCGTTTCTTTGTCTCTGGTCAACAAGAAA 60
X
X 1 GCGGGTGGCGGCAAGGTTGGCGCGCGCGTTTCTTTGTCTCTGGTCAACAAGAAA 60

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1141 GCTTTGAGCCCTCTATGCCGAAGTCTGAGGTGGTAGGAGAAACTCCACGACCGAG 1200
1201 AGGAGGTCACAGAGGTTCTCTATGCTTCTCTACTATTATGACCGAGCTGTGACA 1260
1201 AGGAGGTCACAGAGGTTCTCTATGCTTCTCTACTATTATGACCGAGCTGTGACA 1260
1261 CAGACATGATTGATTATGAAAAGGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAG 1320
1261 CAGACATGATTGATTATGAAAAGGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAG 1320
1321 CCAGGGAAGTGTGTGATACTTCGAAAACCTCACCTCAGGAGTCCCTTCTCTGTCATGG 1380
1321 CCAGGGAAGTGTGTGATACTTCGAAAACCTCACCTCAGGAGTCCCTTCTCTGTCATGG 1380
1381 ATCTCAGCTACATCACAGCCCTGTTTAAAGGATGGCTTTGGCTTTGACAGACAGAGTCT 1440
1381 ATCTCAGCTACATCACAGCCCTGTTTAAAGGATGGCTTTGGCTTTGACAGACAGAGTCT 1440
1441 TACAG 1445
1441 TACAG 1445

```

RESULT 6
 AF63384
 D AAF63384 standard; CDNA: 1601 BP.
 X AAF63384;
 C 14-MAY-2001 (first entry)
 X Human cDNA encoding CD39 like protein CD39-L4.
 E Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
 W myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
 M cerebral artery thrombosis; platelet aggregation; inflammation;
 M apoptosis; autoimmune disorder; neurological disorder;
 M Alzheimer's disease; Parkinson's disease; cancer; CD39-L4; ss.
 K Homo sapiens.
 X S
 X WO200110205-A1.
 X 15-FEB-2001.
 D 09-AUG-2000; 2000WO-US21790.
 E 09-AUG-1999; 99US-0370265.
 R 11-JAN-2000; 2000US-0481238.
 R 25-APR-2000; 2000US-0557600.
 R 26-MAY-2000; 2000US-0583231.
 R 30-JUN-2000; 2000US-0608285.
 X (HYSE-) HYSEQ INC.
 A Ford J, Mulero JJ, Yeung G;
 X MPI: 2001-147489/15.
 R P-PSDB; AAB72239.
 X Polynucleotides encoding human CD39-like polypeptides, with apyrase
 R and/or NDPase activity, which are useful in the treatment of
 R pathological conditions caused by thrombosis (e.g. myocardial
 I infarction) and inflammatory disorders -
 I Claim 10; Page 156-157; 203pp; English.
 X This invention relates to polynucleotides encoding human CD39-like
 X polypeptides with apyrase and/or NDPase activity. The polypeptides having
 C ATPase, including NDPase, activity are useful for inhibiting platelet
 C function and can therefore be used in the prophylaxis or treatment of
 C pathological conditions caused by or involving thrombosis or excessive

```

CC coagulation or excessive platelet aggregation, such as myocardial
CC infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
CC artery thrombosis or intracardiac thrombosis, and conditions associated
CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
CC modulating disease states (including platelet aggregation, inflammation
CC and apoptosis) associated with ADP or other purinergic signalling by
CC reducing the levels of NDPs. The polypeptides are also useful for
CC prophylaxis or treatment of inflammation related disorders, such as
CC disorders involving sepsis or systemic inflammatory response syndrome or
CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,
CC cytokine overstimulation); autoimmune disorders such as thrombosis,
CC atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,
CC cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis;
CC neurological disorders including neurodegenerative diseases, epilepsy,
CC depression, Alzheimer's disease, Parkinson's disease, Huntington's
CC disease, and amyotrophic lateral sclerosis; and cancer. The present
CC sequence represents cDNA encoding CD39 like protein CD39-L4.
XX
SQ Sequence 1601 BP; 436 A; 352 C; 428 G; 385 T; 0 other;

Query Match      80.3%; Score 1445; DB 22; Length 1601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGGCTGCGCGCAAGGGTGGCGCGCGCGTTCCTTGTCTGGTCAACAAGAA 60
DB 1 GCGGGCTGCGCGCAAGGGTGGCGCGCGCGTTCCTTGTCTGGTCAACAAGAA 60
QY 61 TGTGAGTGTCTTGGTGAATCCTCATACAGACAAGATCATTTATGGTGTGTAGTTGA 120
DB 61 TGTGAGTGTCTTGGTGAATCCTCATACAGACAAGATCATTTATGGTGTGTAGTTGA 120
QY 121 AAAGTGCATATAAAGGAACCAAGAGAAATTCAGAGGAAGAAATAATGGCTCT 180
DB 121 AAAGTGCATATAAAGGAACCAAGAGAAATTCAGAGGAAGAAATAATGGCTCT 180
QY 181 GCAGGTGTGCGAGCAGGATTCCTTCGCAACAAGAGCTCCACCCAGCCACATCTGGGA 240
DB 181 GCAGGTGTGCGAGCAGGATTCCTTCGCAACAAGAGCTCCACCCAGCCACATCTGGGA 240
QY 241 AAAGATGGCCACTTCTTTGGGGCACAGTCTTTTCTATGCTGGTGGTATCTGTGTGCA 300
DB 241 AAAGATGGCCACTTCTTTGGGGCACAGTCTTTTCTATGCTGGTGGTATCTGTGTGCA 300
QY 301 GCGCTGTCTCCACAGGAACACAGACACTTGGTTGGGGGTATCTTCTCTGTTCATGT 360
DB 301 GCGCTGTCTCCACAGGAACACAGACACTTGGTTGGGGGTATCTTCTCTGTTCATGT 360
QY 361 GCCCATCAATGTACGCCAGCACCTTGTATGGAATTAATGTTGATGAGGAGCACTG 420
DB 361 GCCCATCAATGTACGCCAGCACCTTGTATGGAATTAATGTTGATGAGGAGCACTG 420
QY 421 GAATCGAATTCATGTTTACACCTTTGTGAGAAATGCGCAGGACAGCTTCCAAATCTAG 480
DB 421 GAATCGAATTCATGTTTACACCTTTGTGAGAAATGCGCAGGACAGCTTCCAAATCTAG 480
QY 481 AAGGGGAAGTTTTTGATTCTGTGAAGCCAGSACTTCTGCTTTTGTAGATCAACCTTAAGC 540
DB 481 AAGGGGAAGTTTTTGATTCTGTGAAGCCAGSACTTCTGCTTTTGTAGATCAACCTTAAGC 540
QY 541 AGGTGTCTGAGACCGTTTCAAGGGCTCTTAGAGTGGCCAAAGACTCAATCCCGGAGTC 600
DB 541 AGGTGTCTGAGACCGTTTCAAGGGCTCTTAGAGTGGCCAAAGACTCAATCCCGGAGTC 600
QY -601 ACTGGAAGAGCCCGAGTGGTCTTAAGGCAACAGCAGGACTACCGTTACTGCCGAGAC 660
DB 601 ACTGGAAGAGCCCGAGTGGTCTTAAGGCAACAGCAGGACTACCGTTACTGCCGAGAC 660
QY 661 ACAAGGCAAGGCTCTCTCTTTGAGTAAAGGAGATCTTCAGGAACTACCTTTCTCTGG 720
DB 661 ACAAGGCAAGGCTCTCTCTTTGAGTAAAGGAGATCTTCAGGAACTACCTTTCTCTGG 720
QY 721 TACCAAGGGGAGTGTGTAGCATCATGATCGATCCGAGGAAGGCATATTAGCTTGGTTA 780

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721 TACCAAGGCGAGTGTAGCATCATGGATGGATCCGACGAGGACATATTAGCTTGGGTTA 780
 781 CTGTGAATTTCTGACAGGTGAGTGCATGGCCACAGACGAGGAGCTGTGGGACCTTGG 840
 781 CTGTGAATTTCTGACAGGTGAGTGCATGGCCACAGACGAGGAGCTGTGGGACCTTGG 840
 841 ACTAGGGGAGGCTCCACCAATACAGTTCTCTGCCAGTTTACGAAATCTCTGGAAC 900
 841 ACTAGGGGAGGCTCCACCAATACAGTTCTCTGCCAGTTTACGAAATCTCTGGAAC 900
 901 AACTCTCTAGGGCTTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
 901 AACTCTCTAGGGCTTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
 961 CACATAGTTTACCTTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTTGGGAGCCCTGG 1020
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 1021 AGACAGAGGAGTGTATGGGACACTTCCGAGTGCCTGTTTACCGAGATGGTTGGAAG 1080
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 1141 GCTTTGAGCCCTGCTATGCGAAGTGTGAGGGTGTGACGAGGAAACTTACACGAGCCAG 1200
 1141 GCTTTGAGCCCTGCTATGCGAAGTGTGAGGGTGTGACGAGGAAACTTACACGAGCCAG 1200
 1201 AGAGTGTGAGAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1260
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 1321 CCAGGGAAGTGTGTATACTTGGAAACTTCACTCTCAGGAGTCTCTCTCTCTCTCTCT 1380
 1321 CCAGGGAAGTGTGTATACTTGGAAACTTCACTCTCAGGAGTCTCTCTCTCTCTCTCT 1380
 1381 ATCTCAGTACATCAGAGCCCTGTTAAAGAGTGGCTTTGGCTTTGCAGACAGCAGTCT 1440
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 1441 TACAG 1445
 1441 TACAG 1445

RESULT 7
 AF63402

AAF63402 standard; DNA; 1287 BP.

AAF63402;

14-MAY-2001 (first entry);

Human CD39 like protein CD39-L4 coding sequence.

Human CD39-like protein; apyrase; NDase; platelet function inhibitor; myocardial infarction; cerebral ischaemia; angina; arterial thrombosis; cerebral artery thrombosis; platelet aggregation; inflammation; apoptosis; autoimmune disorder; neurological disorder; Alzheimer's disease; Parkinson's disease; cancer; CD39-L4; ds.

Homo sapiens.

WO200110205-A1.

15-FEB-2001.

XX PF 09-AUG-2000; 2000WO-US21790.
 XX PR 09-AUG-1999; 99US-0370265.
 PR 11-JAN-2000; 2000US-0481238.
 PR 25-APR-2000; 2000US-0557800.
 PR 26-MAY-2000; 2000US-0583231.
 PR 30-JUN-2000; 2000US-0608285.
 XX (HYSE-) HYSEQ INC.
 XX Ford J, Mulero JJ, Yeung G,
 PI WPI; 2001-147489/15.
 XX P-FSD3; AAB72243.
 DR Polynucleotides encoding human CD39-like polypeptides, with apyrase
 PT and/or NDase activity, which are useful in the treatment of
 PT pathological conditions caused by thrombosis (e.g. myocardial
 PT infarction) and inflammatory disorders -
 XX Disclosure; Page 140-142; 203pp; English.
 XX This invention relates to polynucleotides encoding human CD39-like
 CC polypeptides with apyrase and/or NDase activity. The polypeptides having
 CC ATPase, including NDase, activity are useful for inhibiting platelet
 CC function and can therefore be used in the prophylaxis or treatment of
 CC pathological conditions caused by or involving thrombosis or excessive
 CC coagulation or excessive platelet aggregation, such as myocardial
 CC infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
 CC artery thrombosis or intracardiac thrombosis, and conditions associated
 CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
 CC modulating disease states (including platelet aggregation, inflammation
 CC and apoptosis) associated with ADP or other purinergic signalling by
 CC reducing the levels of NTPs. The polypeptides are also useful for
 CC prophylaxis or treatment of inflammation related disorders, such as
 CC disorders involving sepsis or systemic inflammatory response syndrome or
 CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,
 CC cytokine overstimulation); autoimmune disorders such as thrombosis,
 CC atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,
 CC cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis;
 CC neurological disorders including neurodegenerative diseases, epilepsy,
 CC depression, Alzheimer's disease, Parkinson's disease, Huntington's
 CC disease, and amyotrophic lateral sclerosis; and cancer. The present
 CC sequence represents the CD39 like protein CD39-L4 coding sequence.
 XX Sequence 1287 BP; 330 A; 290 C; 344 G; 323 T; 0 other;

Query Match 71.5%; Score 1287; DB 22; Length 1287;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 ATGGCCACTTCTTGGGGCACAGCTTTTTCATGCTGGTGGTATCTTCTGTTCCATGTTGCGGCT 305
 Db 1 ATGGCCACTTCTTGGGGCACAGCTTTTTCATGCTGGTGGTATCTTCTGTTTGCAGGCT 60
 QY 306 GTCTCCACAGGAACCCAGCAGCTTGGTTTGGGGTATCTTCTGTTCCATGTTGCGGCT 365
 Db 61 GTCTCCACAGGAACCCAGCAGCTTGGTTTGGGGTATCTTCTGTTTCCATGTTGCGGCT 120
 QY 366 ATCAATGTCAGCGCCAGCAGCTTGTATGGAATATGTTGATGTCAGGGAGCAGTGAAC 425
 Db 121 ATCAATGTCAGCGCCAGCAGCTTGTATGGAATATGTTGATGTCAGGGAGCAGTGAAC 180
 QY 426 CGAATTCATGTTTACACCTTTGTGCGAGAAATCCAGGAGCAGCTTCCAAATCTTAGAGGG 485
 Db 181 CGAATTCATGTTTACACCTTTGTGCGAGAAATCCAGGAGCAGCTTCCAAATCTTAGAGGG 240
 QY 486 GAAAGTTTTGATTTCTGTAGCGCAGCAGCTTCTGCTTTTGTAGATCAACCTAAGCAGGGT 545
 Db 241 GAAAGTTTTGATTTCTGTAGCGCAGCAGCTTCTGCTTTTGTAGATCAACCTAAGCAGGGT 300
 QY 546 GCTGAGACCGCTTCAAGGGCTCTTAGAGGTGGCCAAAGACTTCAATCCCCCGAAGTCACTGG 605

301 GCTGAGACCGTTCAAGGCGCTTTAGAGGTGGCCAAAGACTCAATCCCCGAAGTCACTGG 360

606 AAAAAGACCCCACTGGTCTTAAAGGCAACAGCAGACTACGCTTACTTGCAGAACACAA 665

361 AAAAAGACCCCACTGGTCTTAAAGGCAACAGCAGACTACGCTTACTTGCAGAACACAA 420

666 GCCAAGGCTCTGCTTTTGAAGGTAAAGAGATCTTGAAGAGTCACTTTCCTTGGTACCA 725

421 GCCAAGGCTCTGCTTTTGAAGGTAAAGAGATCTTGAAGAGTCACTTTCCTTGGTACCA 480

726 AAGGCACTGTAGCATCATGGATGCGACGAAGGSCATATTAGCTTGGGTACTGTG 785

481 AAGGCACTGTAGCATCATGGATGCGACGAAGGSCATATTAGCTTGGGTACTGTG 540

786 AATTTTCTGACAGGTCACTGCATGGCCACAGACGAGACTGTGGGACCTTGGACCTA 845

541 AATTTTCTGACAGGTCACTGCATGGCCACAGACGAGACTGTGGGACCTTGGACCTA 600

846 GGGGAGGCTCCACCAATCAGCTTCTGCCCCAGTTTGAGANAATCTTGGACAACCT 905

601 GGGGAGGCTCCACCAATCAGCTTCTGCCCCAGTTTGAGANAATCTTGGACAACCT 660

906 CCTAGGGCTACCTCACATTCCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACAT 965

661 CCTAGGGCTACCTCACATTCCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACAT 720

966 AGTTACCTGGGATTTGGATTTGAAGCTGCAAGACTAGCAACCTTGGAGGCTTGGAGACA 1025

721 AGTTACCTGGGATTTGGATTTGAAGCTGCAAGACTAGCAACCTTGGAGGCTTGGAGACA 780

1026 GAAGGCACTGATGGGCACACTTTCGGAGTGCCTGTTTACCGAGATGGTTTGGGAAGCAGAG 1085

781 GAAGGCACTGATGGGCACACTTTCGGAGTGCCTGTTTACCGAGATGGTTTGGGAAGCAGAG 840

1086 TGGATCTTTGGGGTGTGAANATACAGTATGCTGGCAACCAAGAGGGGAGGTGGGCTTT 1145

841 TGGATCTTTGGGGTGTGAANATACAGTATGCTGGCAACCAAGAGGGGAGGTGGGCTTT 900

1146 GAGCCCTGCTATGCCGAAGTCTGAGGGTGTGACGAGAAACTTCAACAGCAGAGGAG 1205

901 GAGCCCTGCTATGCCGAAGTCTGAGGGTGTGACGAGAAACTTCAACAGCAGAGGAG 960

1206 GTCCAGAGAGGTTCCTTCTATGCTTCTCTTACTATATGACCGAGCTGTGTGACACAGAC 1265

961 GTCCAGAGAGGTTCCTTCTATGCTTCTCTTACTATATGACCGAGCTGTGTGACACAGAC 1320

1266 ATGATTGATTATGAAGGGGGGTATTTTAAAGTTGGAAGATTTTGAAGAAAGCCAGG 1325

1021 ATGATTGATTATGAAGGGGGGTATTTTAAAGTTGGAAGATTTTGAAGAAAGCCAGG 1380

1326 GAAGTGTGTGATTAACCTTGGAAAACCTTCACTCAGGAGTCCCTTTCCTGTGCATGGATCTC 1385

1081 GAAGTGTGTGATTAACCTTGGAAAACCTTCACTCAGGAGTCCCTTTCCTGTGCATGGATCTC 1140

1386 AGCTACATCACAGCCCTGTTTAAAGGATGGCTTTGGCTTTGAGACAGCAGACTCTTACAG 1445

1141 AGCTACATCACAGCCCTGTTTAAAGGATGGCTTTGGCTTTGAGACAGCAGACTCTTACAG 1500

1446 CTCACAAAGAAAGTGAACAAACATAGAGACGGGCTTGGGCTTTGGGGGCCACCTTTCACCTG 1505

1201 CTCACAAAGAAAGTGAACAAACATAGAGACGGGCTTGGGCTTTGGGGGCCACCTTTCACCTG 1260

1506 TTGCAGTCTCTGGGCATCTCCCAATGA 1532

1261 TTGCAGTCTCTGGGCATCTCCCAATGA 1287

XX	18-MAY-2000	(first entry)
XX	Human CD39-L4 variant-ACR III mutant protein encoding cDNA.	
XX	CD39-L4; human; apyrase; nucleotide diphosphatase; NDPase; variant;	
XX	ATP Diphosphohydrolase; ATPase; adenosine diphosphate; ADP; treatment;	
XX	platelet aggregation; antithrombotic; thrombosis; myocardial infarction;	
XX	cerebral ischaemia; angina; vascular graft; extracorporeal circulation;	
XX	molecular weight marker; nutritional supplement; tumour; prevention;	
XX	drug targeting; substitution mutation; ss.	
XX	Homo sapiens.	
XX	Key	
XX	Location/Qualifiers	
XX	1..1287	
XX	/*tag= a	
XX	/product= "Human CD39-L4 variant-ACR III mutant protein"	
XX	replace (502..503, GA)	
XX	/*tag= b	
XX	old_sequence	
XX	replace (508..510, TCC)	
XX	/*tag= c	
XX	old_sequence	
XX	replace (525, A)	
XX	/*tag= d	
XX	WO200004041-A2.	
XX	27-JAN-2000.	
XX	16-JUL-1999; 99WO-US16180.	
XX	16-JUL-1998; 98US-0118205.	
XX	24-JUL-1998; 98US-0122449.	
XX	04-FEB-1999; 99US-0244444.	
XX	19-MAR-1999; 99US-0273447.	
XX	09-JUL-1999; 99US-0350836.	
XX	(HYSE-) HYSEQ INC.	
XX	Ford J, Xulero J;	
XX	WPI: 200C-182397/16.	
XX	P-PSDB; AAY44850.	
XX	New nucleic acid encoding human CD39-like protein, useful for treating	
XX	and preventing thrombotic disease -	
XX	Example 9; Fig 6; 125pp; English.	
XX	The present sequence is a cDNA encoding the CD39-L4 variant, designated	
XX	as ACR I11 mutant protein, an apyrase and/or nucleotide diphosphatase	
XX	(NDPase). It is isolated from the human foetal liver-spleen cDNA library,	
XX	b2HFLS20W. It is a soluble ATP Diphosphohydrolases (ATPase) and is	
XX	involved in the hydrolysis of adenosine diphosphate (ADP), the agonist	
XX	that causes platelet aggregation. CD39-L4 protein has 30% and 80%	
XX	homology to human and murine CD39. It has platelet aggregation inhibition	
XX	and antithrombotic activity. CD39-L4 is used to treat or prevent	
XX	thrombosis, myocardial infarction, cerebral ischaemia and angina. It is	
XX	also used in vitro, to maintain vascular grafts or during extracorporeal	
XX	circulation, to hydrolyse NDP, as molecular weight markers and as	
XX	nutritional supplements. It is used to identify therapeutic agents that	
XX	bind and modulate CD39-L4. It is coupled to toxins for targeting drugs	
XX	to tumours or other cells that express CD39-L4.	
XX	Sequence 1287 BP; 331 A; 291 C; 343 G; 322 T; 0 other;	

306 GTCTCCACAGAACAGCAGACTTGGTTTGGAGGTATCTTCTGTCTTCCATGTGCCCC 365
b
61 GTCTCCACAGAACAGCAGACTTGGTTTGGAGGTATCTTCTGTCTTCCATGTGCCCC 120
y
366 ATCAATGTGAGCGCCAGCACCCTGTATGGAAATATGTTTGTATGCCAGGAGCACTGGAAT 425
b
121 ATCAATGTGAGCGCCAGCACCCTGTATGGAAATATGTTTGTATGCCAGGAGCACTGGAAT 180
y
426 CGAATTCATCTTTACACCTTTGTGCAGNAATGCCAGGACAGCTTCCAATCTTAGAAGG 485
b
181 CGAATTCATCTTTACACCTTTGTGCAGNAATGCCAGGACAGCTTCCAATCTTAGAAGG 240
y
486 GAAGTTTGTGATCTGTGAAGCCAGGACTTTCTGCTTTGTATAGTCAACCTTAAGCAGGT 545
b
241 GAAGTTTGTGATCTGTGAAGCCAGGACTTTCTGCTTTGTATAGTCAACCTTAAGCAGGT 300
y
546 GCTGAGACCGTTCAAGGGCTTTAGAGGTGCCAAGACTCAATCCCGAAGTCACTGG 605
b
301 GCTGAGACCGTTCAAGGGCTTTAGAGGTGCCAAGACTCAATCCCGAAGTCACTGG 360
y
606 AAAAAAGCCCGAGTGTCTTAAAGGCAACAGCAGGACTACGTTTACTGCAGAACACAA 665
b
361 AAAAAAGCCCGAGTGTCTTAAAGGCAACAGCAGGACTACGTTTACTGCAGAACACAA 420
y
666 GCCAAGGCTCTGCTTTTGAAGTAAAGGAGATCTTCAGGAAGTCACCTTTCTCTGTACCA 725
b
421 GCCAAGGCTCTGCTTTTGAAGTAAAGGAGATCTTCAGGAAGTCACCTTTCTCTGTACCA 480
y
726 AAGGCGAGTGTAGCATCATGATGATGATCCGAGGAAGGATATAGTTGGGTACTGTG 785
b
481 AAGGCGAGTGTAGCATCATGATGATGATCCGAGGAAGGATATAGTTGGGTACTGTG 540
y
786 AATTTCTGACAGTCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 845
b
541 AATTTCTGACAGTCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
y
846 GGGGAGCCTCCACCAATCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 905
b
601 GGGGAGCCTCCACCAATCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
y
906 CCTAGGGCTCACTCACTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 965
b
661 CCTAGGGCTCACTCACTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 720
y
966 AGTTACCTGGGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1025
b
721 AGTTACCTGGGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
y
1026 GAGGGAGCTGATGGGCACACTTTCGGAGTGCCTGTTTACCGAGATGGTTGGAAGCAGAG 1085
b
781 GAGGGAGCTGATGGGCACACTTTCGGAGTGCCTGTTTACCGAGATGGTTGGAAGCAGAG 840
y
1086 TGGATCTTTGGGGGTGTAATACCACTATGGTGGCAACCAAGAGGGAGGTGGCTTT 1145
b
841 TGGATCTTTGGGGGTGTAATACCACTATGGTGGCAACCAAGAGGGAGGTGGCTTT 900
y
1146 GAGCCCTGCTATGCCAAGTGTCTGAGGGTGTACGAGGAAACTTCCACAGCCAGAGGAG 1205
b
901 GAGCCCTGCTATGCCAAGTGTCTGAGGGTGTACGAGGAAACTTCCACAGCCAGAGGAG 960
y
1206 GTCAGAGAGGTCTCTTATGCTTCTTATGCTTCTTATGCTTATGCTTATGCTTATGCT 1265
b
961 GTCAGAGAGGTCTCTTATGCTTCTTATGCTTCTTATGCTTATGCTTATGCTTATGCT 1020
y
1266 ATGATTCATTAAGAGGGGGGTATTTAAAGTTGAAGATTTGAAGAAAGGAGGAG 1325
b
1021 ATGATTCATTAAGAGGGGGGTATTTAAAGTTGAAGATTTGAAGAAAGGAGGAG 1080
y
1326 GAAGTGTGTGATTAACCTTGGAAACTTCACTCAGGAGTCTTCTGCTGCTGCTGCTGCT 1385
b
1081 GAAGTGTGTGATTAACCTTGGAAACTTCACTCAGGAGTCTTCTGCTGCTGCTGCTGCT 1140

QY 1386 AGTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCAGTCTTACAG 1445
Db
1141 AGTACATCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGCAGACAGCAGTCTTACAG 1200
QY 1446 CTCACAAAGAAAGTGAACACATAGACAGCGGCTTGGGCTTTGGGGCCACCTTTCACCTG 1505
Db
1201 CTCACAAAGAAAGTGAACACATAGACAGCGGCTTGGGCTTTGGGGCCACCTTTCACCTG 1260
QY 1506 TTGAGTCTCTGGGCACTCTCCATTGA 1532
Db
1261 TTGAGTCTCTGGGCACTCTCCATTGA 1287
RESULT 9
AAF63385
ID AAF63385 standard; DNA; 1287 BP.
XX AAF63385;
XX 14-MAY-2001 (first entry)
XX DNA encoding human CD39 like protein CD39-L4 variant ACR11.
DE Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
XX myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
KW cerebral artery thrombosis; platelet aggregation; inflammation;
KW apoptosis; autoimmune disorder; neurological disorder; mutant;
KW Alzheimer's disease; Parkinson's disease; cancer; CD39-L4; ds.
XX Homo sapiens.
OS Synthetic.
XX WC20C110205-A1.
XX 15-FEB-2001.
XX 09-AUG-2000; 2000MO-US21790.
PF 09-AUG-1999; 99US-0370265.
PR 11-JAN-2000; 2000US-0481238.
PR 25-APR-2000; 2000US-0557800.
PR 26-MAY-2000; 2000US-0583231.
PR 30-JUN-2000; 2000US-0608285.
XX (HYSE-) HYSEQ INC.
XX Ford J, Mulero JJ, Yeung G;
PI WPI; 2001-147489/15.
DR P-PSDB; AAB72240.
XX Polynucleotides encoding human CD39-like polypeptides, with apyrase
PT and/or NDPase activity, which are useful in the treatment of
PT pathological conditions caused by thrombosis (e.g. myocardial
PT infarction) and inflammatory disorders -
XX
PS Example 9; Fig 6; 203pp; English.
XX This invention relates to polynucleotides encoding human CD39-like
CC polypeptides with apyrase and/or NDPase activity. The polypeptides having
CC ATPase, including NDPase, activity are useful for inhibiting platelet
CC function and can therefore be used in the prophylaxis or treatment of
CC pathological conditions caused by or involving thrombosis or excessive
CC coagulation or excessive platelet aggregation, such as myocardial
CC infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
CC artery thrombosis or intracardiac thrombosis, and conditions associated
CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
CC mediating disease states (including platelet aggregation, inflammation
CC and apoptosis) associated with ADP or other purinergic signalling by
CC reducing the levels of NDPs. The polypeptides are also useful for
CC prophylaxis or treatment of inflammation related disorders, such as
CC disorders involving sepsis or systemic inflammatory response syndrome or
CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,

cytokine overstimulation); autoimmune disorders such as thrombosis, atherosclerosis, acute pancreatitis, dermatitis, including psoriasis, cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis; neurological disorders including neurodegenerative diseases, epilepsy, depression, Alzheimer's disease, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis; and cancer. The present sequence represents DNA encoding variant ACR111 of human CD39 like protein CD39-L4.

Sequence 1287 BP; 331 A; 291 C; 343 G; 322 T; 0 other;

Query Match 71.0%; Score 1277.4; DB 22; Length 1287;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 1281; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

246 ATGGCCACTCTTGGGGCACAGCTCTTTTCATGCTGGTATCTCTGTGTTGAGCGCT 305

1 ATGGCCACTCTTGGGGCACAGCTCTTTTCATGCTGGTATCTCTGTGTTGAGCGCT 60

306 GTCTCCACAGAACACAGACTTGGTTGAGGGTATCTTCCTGTCTTCATGTGCCCC 365

61 GTCTCCACAGAACACAGACTTGGTTGAGGGTATCTTCCTGTCTTCATGTGCCCC 120

366 ATCATGTACAGCGCCAGCACTTGTATGGATATGTTGATGAGGAGCACTTGAAC 425

121 ATCATGTACAGCGCCAGCACTTGTATGGATATGTTGATGAGGAGCACTTGAAC 180

426 CGAATTCATGTTTACACCTTTGTGCAGAAATGCCAGACAGCTTCCAATTCAGAAGG 485

181 CGAATTCATGTTTACACCTTTGTGCAGAAATGCCAGACAGCTTCCAATTCAGAAGG 240

486 GAAGTTTGTGTCGACGCGAGCTTCTGCTTTTGTAGATCAACCTTAGCAGGCT 545

241 GAAGTTTGTGTCGACGCGAGCTTCTGCTTTTGTAGATCAACCTTAGCAGGCT 300

546 GCTGAGACCGTCTCAAGGGCTCTTAGAGTGCCCAAGACTCAATCCCGCAAGTCACTGG 605

301 GCTGAGACCGTCTCAAGGGCTCTTAGAGTGCCCAAGACTCAATCCCGCAAGTCACTGG 360

606 AAAAGACCCAGTGGTCTTAAAGCAACACAGAGACTACGCTTACTGCCAGAACAA 665

361 AAAAGACCCAGTGGTCTTAAAGCAACACAGAGACTACGCTTACTGCCAGAACAA 420

666 GCCAGGCTCTGCTCTTTGAGTAAGAGATCTCAGGAGTCACTTCTCGGTACCA 725

421 GCCAGGCTCTGCTCTTTGAGTAAGAGATCTCAGGAGTCACTTCTCGGTACCA 480

726 AAGGCACTGTAGCATCATGATGCCAGCAAGGCAATATTAGTCTGGTACTGTG 785

481 AAGGCACTGTAGCATCATGATGCCAGCAAGGCAATATTAGTCTGGTACTGTG 540

786 AATTTCTGACAGGTACGCTGCATGGCCACAGACAGAGACTGTGGGACCTTGGACCTA 845

541 AATTTCTGACAGGTACGCTGCATGGCCACAGACAGAGACTGTGGGACCTTGGACCTA 600

846 GGGGAGGCTCCACCCAAATCACGTTCTGCCCCAGTTTGAGAAATCTCGGAACAACT 905

601 GGGGAGGCTCCACCCAAATCACGTTCTGCCCCAGTTTGAGAAATCTCGGAACAACT 660

906 CTTAGGGCTACCTCACTCTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACAT 965

661 CTTAGGGCTACCTCACTCTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACAT 720

966 AGTTACCTGGGATTTGGATTGAAGCTGCAAGACTAGCAACCTCGGAGCCCTGGAGCA 1025

721 AGTTACCTGGGATTTGGATTGAAGCTGCAAGACTAGCAACCTCGGAGCCCTGGAGCA 780

1026 GAAGGAGCTGATGGGCACACTTCCGAGTGTCTTTTACCAGATGTTTGGAGACAGAG 1085

781 GAAGGAGCTGATGGGCACACTTCCGAGTGTCTTTTACCAGATGTTTGGAGACAGAG 840

1086 TGGATCTTTGGGGTGTGAAATACAGTATGTTGGCAACCAAGAGGGGAGGTGGGCTTT 1145

84: TGGATCTTTGGGGTGTGAAATACCATATGTTGGCAACCAAGAGGGAGGTGGGCTTT 900

1146 GAGCCCTGCTATGCCGAAGTGTCTGAGGGTGTACGAGGAAACTTCCACGACAGAGGAG 1205

901 GAGCCCTGCTATGCCGAAGTGTCTGAGGGTGTACGAGGAAACTTCCACGACAGAGGAG 960

1206 GTCCAGAGAGTCTCTTCTATGCTTTCTTACTATTATACAGGCTGTGACACAGAC 1265

961 GTCCAGAGAGTCTCTTCTATGCTTTCTTACTATTATACAGGCTGTGACACAGAC 1020

1266 ATGATTGATTATGAAAGGGGGTATTTTAAAGTTGAAGTATTGAAAGAAAGCCAGG 1325

1021 ATGATTGATTATGAAAGGGGGTATTTTAAAGTTGAAGTATTGAAAGAAAGCCAGG 1080

1326 GAAGTGTGTGATAACTTTGGAAACTTCCACCTCAGGAGTCTTTCCTGTGCATGGATCTC 1385

1081 GAAGTGTGTGATAACTTTGGAAACTTCCACCTCAGGAGTCTTTCCTGTGCATGGATCTC 1140

1386 AGTACATACAGCCCTGTTTAAAGTATGGCTTTGCGACACAGCAGTCTTACAG 1445

1141 AGTACATACAGCCCTGTTTAAAGTATGGCTTTGCGACACAGCAGTCTTACAG 1200

1446 CTCACAAAGAAAGTGAACAACATAGACCGGCTTGGGCCCTTGGGGGCCACCTTTCACCTG 1505

1201 CTCACAAAGAAAGTGAACAACATAGACCGGCTTGGGCCCTTGGGGGCCACCTTTCACCTG 1260

1506 TTGAGTCTCTGGGCATCTCCCATTTGA 1532

1261 TTGAGTCTCTGGGCATCTCCCATTTGA 1287

RESULT 10

AAC98093

CD AAC98093 standard; cDNA; 1457 BP.

XX AAC98093;

XX AC

XX XX

DT 09-MAR-2001 (first entry)

XX

DE Human colon cancer antigen nucleotide sequence SEQ ID NO:103.

XX

XX Human; colon cancer; colon cancer antigen; diagnosis; detection;

KW identification; cytostatic; cardioactive; neuroprotective; vulnary;

KW immunomodulatory; muscular; gynaecological; gastrointestinal;

KW nephropathic; anti-infective; antibacterial; gene therapy; wound;

KW neutral disorder; immune system disorder; muscular disorder;

KW reproductive disorder; gastrointestinal disorder; renal disorder;

XX infectious disease; cardiovascular disorder; ss.

OS Homo sapiens.

XX

XX NC020055351-A1.

PN

XX

PD 21-SEP-2000.

XX

PF 08-MAR-2000; 2000WO-US05883.

XX

PR 12-MAR-1999; 99US-0124270.

XX

XX (HUMA-) HUMAN GENOME SCI INC.

PA

XX

PI Rosen CA, Ruben SM;

XX

DR WPI: 2000-587534/55.

XX

XX P-PSDB; AAB53336.

XX

PT Colon cancer associated gene sequences, referred to as colon cancer

PT antigens, useful for the treatment, prevention, and diagnosis of colon

PT disorders such as colon cancer -

XX

PS Claim 1; Page 544; 2104pp; English.

XX

CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,

5 734 A T A A G A A G G G G G T A T T T A A A A G T G A A G A T : : T G A A G A G A A A G C C A G G G A A G T G T 753

2. 5377

CD39L2, u

PT An isolated polypeptide with phosph

An isolated p

T identify inhibitors and for treatment of, e.g., Alzheimer's, multiple
T sclerosis and osteoporosis

X Example; Fig 1; 101pp; English.

X The present invention relates to novel proteins with phosphohydrolase
X activity, designated CD-39-like (CD39L) proteins and polynucleotides
X encoding such proteins. CD39L proteins are useful to treat infectious
X diseases caused by viral, bacterial, fungal or other infection that may
X be treatable with CD39L. They are useful in the treatment of various
X immune deficiencies and disorders, autoimmune disorders such as multiple
X sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune
X thyroiditis and insulin dependent diabetes mellitus, allergic reactions
X and conditions such as asthma and other respiratory problems, periodontal
X disease, osteoporosis, osteoarthritis and other tooth repair processes.
X They may have utility in compositions used for bone, cartilage, tendon,
X ligament and/or nerve tissue growth or regeneration as well as for wound
X healing and tissue repair and replacement and in the treatment of burns.
X incisions and ulcers. CD39L proteins may also be useful for proliferation
X of neural cells and for regeneration of nerve and brain tissue, i.e. for
X the treatment of central nervous system diseases such as Alzheimer's
X disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's
X disease, peripheral nervous system diseases peripheral nerve injuries,
X peripheral neuropathy and localised neuropathies. They are also used to
X treat mechanical and traumatic disorders which involve degeneration,
X death or trauma to neural cells or nerve tissue. CD39L proteins of the
X invention are also useful to promote better or faster closure of non-
X healing wounds, including pressure ulcers, ulcers associated with
X vascular insufficiency and surgical and traumatic wounds. They also
X exhibit anti-inflammatory activity and may be used to treat inflammatory
X conditions including chronic or acute conditions, including ischaemia-
X reperfusion injury, endotoxin lethality, arthritis, nephritis, cytokine
X or chemokine-induced lung injury, inflammatory bowel disease or Crohn's
X disease. The present sequence is a DNA encoding mouse CD39L4 protein,
X also known as nucleotide-triphosphatase (NTPase). CD39L4 gene is
X localised on chromosome 12.

X Sequence 2119 BP; 545 A; 482 C; 546 G; 546 T; 0 other;

Query Match Similarity 58.3%; Score 1C49.6; DB 24; Length 2119;
Best Local Similarity 81.4%; Pred. No. 0;
Matches 1270; Conservative 0; Mismatches 274; Indels 16; Gaps 4;
Y 48 GTCAACAAAGAAATGTGGAGTGTCTGGCTGAATCTCATACACAGAAATCATTA---- 103
D 3 GTTGACACAGGAATCAGAGATGCTATGCTGAATCTTCAAGCAGGCGATATTGACCAT 62
Y 124 ----TGGTGTCTGTAGGTGTGAAAAGTGATATATAAAGAACAGGAGAAATTCAGA 159
b 63 GTGCTTTTAAATTTGGCTGGTACCCGCGCCACTTGGTGTAAAGAAAGAACCGGTCMAA 122
Y 160 AGGAAGAAAGAAATTTGCTCTGCAGGTGTGGAGCAGGATTTCTTCTGCAACAAAGCCT 219
b 123 GGGAGGGCTCAAGGACCTCCACAGGAGTGTGACAGCAGCTGCTTACAGCAACAAG---- 178
Y 220 CCACCCAGCCACATCTTGGGAAAAGATGGCCATCTTTGGGGCAGAGCTTTTTCATGC 279
b 179 CCTCAGGTCCACATCTTGGGAAGAATATGGCCACTTCTCTGGGGGCTGTCTTTCATGC 235
Y 280 TGGTGGTATCTGTGTGGAGCGCTGTCTCCACAGGACAGCAGCAGCTTGGTTGAGG 339
b 236 TGATCATAGCTGGCTGGCAGCATCTTCTTACAGAGAACAGCAGCAGCTGGTTGAAG 295
Y 340 GTATCTTCTGTCTTCCATGTGCCCATCAATGTTCAGCGCCAGCAGCCTTGTATGGAATTA 399
b 256 GTGTCTCTTGTCTTCCATGTGCCCATTAATGTGATGCGGCGACCTTTATGGAATTA 355
Y 400 TGTTTGATGCGAGGAGCACTGGAACTCGAATTCATGTTTACCTTTTGTGAGAAATGC 459
b 356 TGTTTGATGCGGAGCAGCACTGGAGCTCGAATTCATGTTTACACTTTTGTGAGAAACAG 415
Y 460 CAGGACAGCTTCCAAATCTAGAGGGAGTTTGTGATCTGTGAGCCAGGAGCTTCTG 519

416 CAGGACAGCTCCCTTTCTGTGAAGGTGAAATTTTGTGATCTCTGTGAACCCGGGACTTTCTG 475
520 CTTTGTGTAGATCAACCTTAAGCAGGGTCTCTGAGACCGTTCAAGGGCTCTTAGAGTGGCCA 579
476 CTTTGTGTGATCAGCCCAACACAGGGTCTCTGAGACTGTCCAGAGCTCTTGTGAGTGGCCA 535
590 AAGACTCAATCCCCCGAAGTCACTGGGAAAAGACCCAGTGGTCTTAAAGGCAACAGCAG 639
536 AAGACTCGATCCCCAGAAAGCCACTGGGAAAAGGACCCCGTGGTCTTAAAGGCAACCGCCG 595
640 GACTACGCTTACTCCCAAGAACACAAAGCCAGGCTCTGCTCTTTGAGGTAAAGAGATCT 699
596 CACTCCGTTTCTGCTGAGCAGCAAAAGCCAGGCTCTGCTCTTGGAGTAGAGAGATCT 655
700 TCAAGAACTCACTTTTCTGCTACCAAGGGCAGTGTAGCATCATGGATGGATTCGGAAG 759
656 TCAAGAACTCACTTTCTGCTGCTCAGATGCGACGGTAGCATCATGGATGGATTCGCTATG 715
760 AAGCATATTAGCTTGGGTACTGTGAATTTCTGACAGGCTCAGCTGCATGGCCACAGAC 819
716 AAGGATACTAGCTGGGTACCGTGAATTTCTACAGGCTCAGCTGCATGGTGGTGGCC 775
820 AGGAGACTGTGGGACCTTGGACCTAGGGGGAGCCTCCACCCAAATCACGTTCTCTGCCCC 879
776 AGGAGACTGTGGGACCTTGGACCTGGGGGGTGCCTCCACCCAAATCACGTTCTACCCC 835
880 AGTTTGAGAAACTCTGGAACAAACTCTAGGGGCTACCTCACTTCTTTGAGATGTTTA 939
836 AGTTTGAGAAACCTTGGAAACAAACACTAGGGGCTACCTCACTTCTTTGAGATGTTTA 895
940 ACAGCACTTATAAGCTCTATACACATAGTTACCTGGGATTTGGATTGAAAGCTGCAAGAC 999
896 ACAGCACTTTTAAGCTCTATACACATAGTTACTTGGGATTTGGACTGAAAGCTGCAAGAC 955
1000 TAGCAACCTCGGAGCCCTGGAGACAGAGGAGTGTAGTGGSCACACTTTCCGGAGTGCCT 1059
956 TGGCAACTCTGGGAGCCCTGGAAGCAAAAGGGAGCTGATGGACATACGTTTCAAGTGCCT 1015
1060 GTTTACCGAGATGTTGGAAGCAGAGTGGATCTTTGGGGGTGTGAAATACAGTATCGTG 1119
1016 GTTTACCAAGATGTTGGAAGCAGAGTGGATCTTTGGGGGTGTGAAATACAGTATCGTG 1075
1120 GCAACCAAGAAAGGGAGTGGGCTTTGAGCCCTGCTATGCGGAGTGTCTGAGGGTGTATC 1179
1076 GTACCAAGAAAGGGAGATGGCTTTGAAACCTGCTATGCGGAGTGTCTGAGGGTGTATC 1135
1180 GAGGAAACTTCACAGCCAGAGAGGCTCCAGAGAGGTTCTCTTATGCTTCTCTTACT 1239
1136 AGGGAAACTTCACAGCCAGAGAGGCTCCAGAGAGGCTCTACGCTTCTCTTACT 1195
1240 ATTATGACCGAGCTGTTGACACAGACATGATGATTTATGAAAGGGGGGTATTTTAAAG 1299
1196 ACTAGATTCAGGCGCTGACACACACTTATGATCGATTATGAAAGGGGGGTATTTAAAG 1255
1300 TTGAAGATTTGAAAGAAAGCCAGGAGTGTGATTAATTGAAAGAACTTCACTCTCAG 1359
1256 TTGAAGATTTGAAAGAAAGCCAGAGAGTGTGACAACTTTGGGAGGCTTCTCTCTCG 1315
1360 GCAGTCTCTTCTGTCGATGATCTCAGCTACATCAGACCTGTTTAAAGGTGGCTTTG 1419
1316 GCAGTCTCTTCTTCTGATGAGCTCACTTACATCAGCCCTGTTGAAAGATGTTTGG 1375
1420 GCTTTGAGACACAGCAGTCTTACAGCTCACAAGAAAGTGAACAAACATAGAGACGGGC 1478
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1539 GTACTTCTCTGAGACCTTGCATTTTGGCAACACCTTTTAAAGGGGAGGAGAGACCTTAG 1598
1496 GCTCCACTCTGAAGCTTGCATTTCTGAACCATGTTTCTCACAGGAAGGGTGCATCAG 1555

RESULT 12

AAL22957 standard; cDNA; 799 BP.

AA22957; (first entry)

07-DEC-2001 (first entry)
Human breast cancer expressed polynucleotide 15414.

Human; breast cancer; cell marker; cytostatic; ss.

Homo sapiens.

WO200151628-A2.

19-JUL-2001.

10-JAN-2001; 2001WO-US00799.

14-JAN-2000; 2000US-0176077.

14-MAR-2000; 2000US-0189167.

24-MAR-2000; 2000US-0192099.

29-MAR-2000; 2000US-0193480.

15-MAY-2000; 2000US-0205230.

09-JUN-2000; 2000US-0211315.

25-JUL-2000; 2000US-0220534.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Lillie J, Xu Y, Wang Y, Steinmann K;

WPI; 2001-451856/48.

New peptide useful as a marker for the diagnosis of breast cancer

Claim 1; Page 2797; 3695pp; English.

The invention relates to human breast cancer expressed polynucleotides (AAL07544-AA26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterizing treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity.

Sequence 799 BP; 221 A; 167 C; 228 G; 183 T; 0 other;

Query Match 23.1%; Score 415.2; DB 22; Length 799;

Best Local Similarity 90.3%; Pred. No. 2.1e-118;

Matches 455; Conservative 0; Mismatches 48; Indels 1; Gaps 1;

161 GGAAAGAAAATTCCTCTCAGGTGTGAGCAGGATTGCTTCTGCAACAAAGCCCTC 220

199 GGCAGACACAGCAGCCCTCTCAGGTGTGAGCAGGATTGCTTCTGCAACAAAGCCCTC 258

221 CACCGCCGACCTCTGGGAAGAAATGGCCACTCTTGGGGGACAGCTTTTTCATGCT 280

259 CACCGCCGACCTCTGGGAAGAAATGGCCACTCTTGGGGGACAGCTTTTTCATGCT 318

281 GGTGTATCTCTGTGTTTGGCAGCGTGTCTCCACAGGAACACAGACTTGGTTGAGGG 340

319 GGTGTATCTCTGTGTTTGGCAGCGTGTCTCCACAGGAACACAGACTTGGTTGAGGG 378

341 TATCTCTCTGCTTCCATGTGCCCATCAATGTTCAGCGCCAGCAGCTTGTATGGAATTAT 400

379 TATCTCTCTGCTTCCATGTGCCCATCAATGTTCAGCGCCAGCAGCTTGTATGGAATTAT 438

401 GTTTGATGACGGGAGCAGTGGAACTCGAATTCATGTTTACACCTTTGTGCAGAAATGCC 460

DB 439 GTTTGATGACGGGAGCAGTGGAACTCGAATTCATGTTTACACCTTTGTGCAGAAATGCC 498

QY 461 AGGACAGCTTCCAATTTCTAGAAAGGGGAAGTTTTTGTATTTCTGTGAAGCAGGACTTTCTGC 520

DB 499 AGGACAGCTTCCAATTTCTAGAAAGGGGAAGTTTTTGTATTTCTGTGAAGCAGGACTTTCTGC 558

QY 521 TTTTGTAGATCAACCTTAAGCAGGGGTGTGAGACCGTTTCAGGGGCTCTTAGAGGTGGCCAA 580

DB 559 TTTTGGAGAACACCTTAAGCCGGGTGTGAAACCCGTCAAGGGGCTTTTAAGGGGGGCAA 618

QY 581 AGACTCAATCCCCGGAAGTCACTGGAAAAAGACCCAGTGTCTTAAAGSCAACAGCAGG 640

DB 613 AGACTTAATCCCCGGAATCCCTGGAAAAAGAACCCCATGTCCTTTAAGSCAACAGCAGG 677

QY 641 ACTAGGCTTACTGCAGAACACAA 664

DB 678 AACTCTTTATTGTGGCAAAACAAAA 701

RESULT 13

ABV43087 standard; cDNA; 488 BP.

AC ABV43087;

DT 16-SEP-2002 (first entry)

DE Human prostate expression marker cDNA 43076.

Human; prostate cancer; cytostatic; carcinogen; pharmaco-dynamic marker; pharmacogenomic marker; gene; ss.

OS Homo sapiens.

XX WO200160860-A2.

PD 23-AUG-2001.

PF 20-FEB-2001; 2001WO-US05171.

PR 17-FEB-2000; 2000US-183319P.

PR 16-MAR-2000; 2000US-189862P.

PR 25-MAY-2000; 2000US-207454P.

PR 09-JUN-2000; 2000US-211314P.

PR 18-JUL-2000; 2000US-219007P.

PR 13-DEC-2000; 2000US-255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Endege WO, Monahan JE;

DR WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer

Claim 1; Page 8603; 11750pp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV02213) of the specification or its complement. (I) is useful for:

- CC (a) assessing whether a patient is afflicted with prostate cancer;
- CC (b) monitoring the progression of prostate cancer in a patient;
- CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
- CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
- CC (e) selecting a composition for inhibiting prostate cancer in a patient;
- CC (f) assessing the prostate cell carcinogenic potential of a compound;
- CC (g) determining whether prostate cancer has metastasized in a patient;
- CC (h) assessing the aggressiveness or indolence of prostate cancer in a

X Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
W pharmacogenomic marker; gene; ss.
X Homo sapiens.
X WO2C0160860-A2.
X 23-AUG-2001.
X 20-FEB-2001; 2001WO-US05171.
X 17-FEB-2000; 200CUS-1833192.
X 16-MAR-2000; 200CUS-1898622.
X 25-MAY-2000; 200CUS-207454P.
X 09-JUN-2000; 200CUS-211314P.
X 18-JUL-2000; 200CUS-219007P.
X 13-DEC-2000; 200CUS-255281P.
X (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
X Schlegel R, Endege WO, Monahan JE;
X WPI; 2001-662795/76.
X Novel isolated nucleic acid molecule associated with cancerous state of
T prostate cells and correlating with presence of prostate cancer, useful
T for detecting presence of prostate cancer, stage of prostate cancer
X Claim 1; Page 5917; 1:750pp; English.
X The invention relates to an isolated nucleic acid molecule (:) comprising
C a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the
C specification or its complement. (I) is useful for:
C (a) assessing whether a patient is afflicted with prostate cancer;
C (b) monitoring the progression of prostate cancer in a patient;
C (c) assessing the efficacy of a test compound to inhibit prostate
C cancer in a patient;
C (d) assessing the efficacy of a therapy for inhibiting prostate cancer
C in a patient;
C (e) selecting a composition for inhibiting prostate cancer in a patient;
C (f) assessing the prostate cell carcinogenic potential of a compound;
C (g) determining whether prostate cancer has metastasized in a patient;
C (h) assessing the aggressiveness or indolence of prostate cancer in a
C patient;
C (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
X Sequence 480 BP; 1:1 A; 107 C; 119 G; 143 T; 0 other;

Query Match 20.2%; Score 363.2; DB 23; Length 480;
Best Local Similarity 91.0%; Pred. No. 2.5e-102;
Matches 386; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

117 TTGAAGAAGTCATATATAAGGAACCAAGAGAAATTCAGAAAGAGAAAGAAATTCG 176
57 TTTTACAGGTGTAATAAAGAGTAGTTGTTCTACTTGTGTCTTGTCTTCTAAGC 116
177 CTCTGCAGGTGTGGAGCAGAGATTGCTTCTGCACAAAAGCTCCACCCAGCCACATCTT 236
117 CTCTGCAGGTGTGGAGCAGAGATTGCTTCTGCACAAATAGCTCCACCCAGCCACATCTT 176
237 GGGAAAGCAATGGGCACCTTCTTGGGGCAGACAGTCTTTTTCATGCTGGTGGTATCCTGTGT 296
177 GGGAAAGCAATGGGCACCTTCTTGGGGCAGACAGTCTTTTTCATGCTGGTGGTATCCTGTGT 236
297 TGCAGCGCTGTCTCCACAGAACCCAGCAGACTTGGTTTGAGGGTATCTTCTGTGTCTCC 356
237 TGCAGCGCTGTCTCCACAGAACCCAGCAGACTTGGTTTGAGGGTATCTTCTGTGTCTCC 296
357 ATGTGCCCCCATCAATGTGACGCCAGCACCTTGTATGGAATTTATGTTGATGACGGGAGC 416
297 ATGTGCCCCCATCAATGTGACGCCAGCACCTTGTATGGAATTTATGTTGATGACGGGAGC 356

QY 417 ACTGGAACCTCGAATTCATGTTTACACTTTGTGAGAAATGCCAGACAGCTTCCAATT 476
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
357 ACTGGAACCTCGAATTCATGTTTACACTTTGTGAGAAATGCCAGACAGCTTCCAATT 416
QY 477 CTAGAAGGGGAAGTTTGTGATTCTGTGAAGCCAGGACTTTCTGCTTTTGTAGTCAACCT 536
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
417 CTAGAAGGGGAAGTTTGTGATTCTGTGAAGCCAGGACTTTCTGCTTTTGTAGTCAACCT 476
QY 537 AAGC 540
Db |||||
477 AAGC 480

Search completed: October 6, 2003, 11:14:53
Job time : 391 secs

JOURNAL Submitted (15-DEC-1997) MAMM, ICRF, 44 Lincoln's Inn Fields, London
FEATURES WC2A 3EX, England, UK
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/mol_type="mRNA"
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/chromosome="14"
/map="14q24"
/cell_type="keratinocyte"
1..1998
/gene="CD39L4"
247..1533
/gene="CD39L4"
/note="NTPase homolog; similar to ecto-ATPase/apyrases"
/codon_start=1
/product="CD39L4"
/protein_id="AAC39885.1"
/db_xref="GI:3335102"
/translation="MATSNQTVFPMLVVSCVSAVSHRNQQTWFEGLFLSSMCPINVS
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KGSVIMDSDEGILAWTVNFTLQQLHQRQETVGTLDLGGASTQITFLPQEFKLE
QTPRGYLSFEMFNSYKLYTHSYLGFGLKAARLALTEGTGHTDGHTRSAFLPRW
LEAWIFGVKYQYGNDEGEVGPFCVAVLRVVRGKLHOPREVORGSFVAFSYVD
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BASE COUNT 557 a 449 c 491 g 501 t
ORIGIN
Query Match 87.5%; Score 1575; DB 9; Length 1998;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1620; Conservative 2; Mismatches 2; Indels 25; Gaps 2;
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DB 1 GCGCGCGCTTTCCTGTGTCCTGTCGTCACAAAGAAATGTGGAGTGTCTGGCTGAATCC 60
QY 84 TCATACAGACAGATCATATGTCGTGT-----AGGTTG 119
DB 61 TCATACAGACAGATCATATGTCGTGTGTAGTAGGACTTGTATCCAGATGTAAAGTTG 120
QY 120 AAAAGTGATATAATAAGGAACCAAGGAGAGAAATTCAGAGGAGAAAGAAATTTGCCCTC 179
DB 121 AAAAGTGATATAATAAGGAACCAAGGAGAGAAATTCAGAGGAGAAAGAAATTTGCCCTC 180
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QY 240 AAAAGATGCGCACTTCTGGGCGACAGTCTTTTTCATGCTGGTGGTATCCTGTGTTTGC 299
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QY 360 TGCCTCATCAATGTGAGCGCCAGCAGCTTGTATGGAATATGTTTGTGAGGGAGCACT 419
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DB 661 CACAAGCCAAAGGCTCTGCTCTTTAGGTTAAGAGAGATCTTCAGGAAGTCACTTTCCTG 720
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DB 781 ACTGTGAATTTTCTGACAGGTCACTGCTGATGGCCACAGACAGGAGACTGTGGGACCTTG 840
QY 840 GACCTAGGGGAGGCTCCACCAATCAGCTTCTGCTGCCCCAGTTTGAGAAACTCTGGAA 899
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QY 900 CAACTCTCTAGGGGCTACCTCACTTCTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTAT 959
DB 901 CAACTCTCTAGGGGCTACCTCACTTCTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTAT 960
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DB 1081 GAGAGTGGATCTTTGGGGGTGTGAATACAGATATGTTGGCAACCAAGAAAGGGAGGTG 1140
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DB 1261 ACAGACATGATGATATGAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAA 1320
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SPS

ALIGNMENTS

Best Local Similarity 10
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Query Match 99.8%; Score 1794.8; DB 4; Length 1799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1799: Conservative 0; Mismatches 0;
Indels 0;

1 CGCGGCTCGCGCGCAAGGCTGGCGCGCGCGCTTCTCTTGTTCCTGGTCAACAAAGAAA 60
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RESULT 2
US-09-350-836B-2
; Sequence 2, Application US/093508365
; Patent No. 6387645
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Giulio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/09/350.936B
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1799

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (246)..(1529)
NAME/KEY: misc_feature
LOCATION: (1718)
OTHER INFORMATION: n = adenine or guanine or cytosine or thymine
S-09-350-836B-2

Query Match				99.8%;	Score 1794.8;	DB 4;	Length 1799;
Best Local Similarity				100.0%;	Pred. No. C;		
Matches 1799;				Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
y	1	CGGGCTGCCGCGCAAGGTTGGCGCGCGCTTTCCTTGTTCTCTGGTCAACAAGAAA	60				
b	1	CGGGCTGCCGCGCAAGGTTGGCGCGCGCTTTCCTTGTTCTCTGGTCAACAAGAAA	60				
y	61	TGTGGAGTGTCTTGGCTGAATCTCTACAGCAAGATCATTTATGGTGTGGTCA	120				
b	61	TGTGGAGTGTCTTGGCTGAATCTCTACAGCAAGATCATTTATGGTGTGGTCA	120				
y	121	AAAGTGCATATAAAGGACCAAGAGAGAAATTCAGAGAGAGAGAGAGAAATTCGCTCT	180				
b	121	AAAGTGCATATAAAGGACCAAGAGAGAAATTCAGAGAGAGAGAGAGAAATTCGCTCT	180				
y	181	GCAGGTGTCGAGCAGATGTCTCTGCAACAAAGCCTCCACCCAGCCACATCTTGGGA	240				
b	181	GCAGGTGTCGAGCAGATGTCTCTGCAACAAAGCCTCCACCCAGCCACATCTTGGGA	240				
y	241	AAAGATGGCCACTTCTTGGGCGACAGCTCTTTTCATGCTGTGGTATCTCTGTGTTTGA	300				
b	241	AAAGATGGCCACTTCTTGGGCGACAGCTCTTTTCATGCTGTGGTATCTCTGTGTTTGA	300				
y	301	GCCTGTCTCCACAGAACCCAGCAGCTTGTGAGGATCTCTCTGCTCTTCCATGT	360				
b	301	GCCTGTCTCCACAGAACCCAGCAGCTTGTGAGGATCTCTCTGCTCTTCCATGT	360				
y	361	GCCCCATCAATGTGAGGCGCAGCAGCTTTGATGGAATTTATGTTGATGAGGAGCAGT	420				
b	361	GCCCCATCAATGTGAGGCGCAGCAGCTTTGATGGAATTTATGTTGATGAGGAGCAGT	420				
y	421	GAATCGAATTCATGTTTACACCTTTGTGAGGATCTCTCTGCTCTTCCATGT	480				
b	421	GAATCGAATTCATGTTTACACCTTTGTGAGGATCTCTCTGCTCTTCCATGT	480				
y	481	AAGGGGAAGTTTGTGATCTGTAAGCCAGGACTTTCTGCTTTGTAGATCAACCTAAGC	540				
b	481	AAGGGGAAGTTTGTGATCTGTAAGCCAGGACTTTCTGCTTTGTAGATCAACCTAAGC	540				
y	541	AGGTGCTGAGACCGTTTCAAGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGGAATC	600				
b	541	AGGTGCTGAGACCGTTTCAAGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGGAATC	600				
y	601	ACTGGAAAAAGACCCAGTGGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCGAGAAC	660				
b	601	ACTGGAAAAAGACCCAGTGGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCGAGAAC	660				
y	661	ACAAAGCCAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAAGAGTCACTTCTCTGG	720				
b	661	ACAAAGCCAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAAGAGTCACTTCTCTGG	720				
y	721	TACCAAGAGGCGAGTGTAGCATCATGGATGATCCGACGAAGGCAATTATAGCTGGGTTA	780				
b	721	TACCAAGAGGCGAGTGTAGCATCATGGATGATCCGACGAAGGCAATTATAGCTGGGTTA	780				
y	781	CTGTGAATTTCTGACAGGTCACTGCATGGCCACAGACAGGAGACTGTGGGGACCTTGG	840				
b	781	CTGTGAATTTCTGACAGGTCACTGCATGGCCACAGACAGGAGACTGTGGGGACCTTGG	840				
y	841	ACCTAGGGGAGCCTCCACCCAAATCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900				
b	841	ACCTAGGGGAGCCTCCACCCAAATCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900				

QY	901	AACTCTAGGGCTACCTCCTTCTTGGATGTTTAAACAGCAGCTTAAAGCTCTATA	960
DB	901	AACTCTAGGGCTACCTCCTTCTTGGATGTTTAAACAGCAGCTTAAAGCTCTATA	960
QY	961	CACATAGTTACCTGGATTTGGATTGAAAGCTCAAGACTAGCAACCTGGAGCCCTGG	1020
DB	961	CACATAGTTACCTGGATTTGGATTGAAAGCTCAAGACTAGCAACCTGGAGCCCTGG	1020
QY	1021	AGCAGAGGAGCTGATGGGACACTTTCGGAGTGCCTGTTTACCGAGATGTTGGAAG	1080
DB	1021	AGCAGAGGAGCTGATGGGACACTTTCGGAGTGCCTGTTTACCGAGATGTTGGAAG	1080
QY	1081	CAGAGTGGATCTTTGGGGGTGTGAAATACCAAGTATGGTGGCAACCAAGAGGGAGGTGG	1140
DB	1081	CAGAGTGGATCTTTGGGGGTGTGAAATACCAAGTATGGTGGCAACCAAGAGGGAGGTGG	1140
QY	1141	GCTTTGAGCCCTGCTATGCCGAAGTGTGAGGGTGGTACGAGGAAACCTTCAACGAGCAG	1200
DB	1141	GCTTTGAGCCCTGCTATGCCGAAGTGTGAGGGTGGTACGAGGAAACCTTCAACGAGCAG	1200
QY	1201	AGGAGTCCACAGAGGTTCTCTATGCTTTCTTACTATATATGACCGAGCTCTTCAACA	1260
DB	1201	AGGAGTCCACAGAGGTTCTCTATGCTTTCTTACTATATATGACCGAGCTCTTCAACA	1260
QY	1261	CAGACATGATTGATTATGAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAG	1320
DB	1261	CAGACATGATTGATTATGAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAG	1320
QY	1321	CCAGGAAAGTGTGATTAACCTTGGAACCTTCACTCAGGAGTCTTCTGCTGATGAG	1380
DB	1321	CCAGGAAAGTGTGATTAACCTTGGAACCTTCACTCAGGAGTCTTCTGCTGATGAG	1380
QY	1381	ATCTCAGCTACATCACAGCCCTGTTAAAGGATGCTTTGGCTTTGACAGACAGCAGTCT	1440
DB	1381	ATCTCAGCTACATCACAGCCCTGTTAAAGGATGCTTTGGCTTTGACAGACAGCAGTCT	1440
QY	1441	TACAGCTCACAAAGAAAGTGAACAAATAGACAGCGGCTGGGCTTTGGGGCCACCTTTC	1500
DB	1441	TACAGCTCACAAAGAAAGTGAACAAATAGACAGCGGCTGGGCTTTGGGGCCACCTTTC	1500
QY	1501	ACCTGTTGAGCTCTTGGGATCTCCCATTTGAGGCGAGCTACTTCTTGGAGACCTGCAT	1560
DB	1501	ACCTGTTGAGCTCTTGGGATCTCCCATTTGAGGCGAGCTACTTCTTGGAGACCTGCAT	1560
QY	1561	TTGCCAACACCTTTTAAAGGGAGGAGAGCAGCTTAGTTTCTGAACTAGTCTGGGAGCA	1620
DB	1561	TTGCCAACACCTTTTAAAGGGAGGAGAGCAGCTTAGTTTCTGAACTAGTCTGGGAGCA	1620
QY	1621	TCCTGGACTTGGAGCTAGAGATTWRGTTAATTAASCGGCGAGCTTATCTTWTATAGGT	1680
DB	1621	TCCTGGACTTGGAGCTAGAGATTWRGTTAATTAASCGGCGAGCTTATCTTWTATAGGT	1680
QY	1681	AATTACTTGTGTCGCGCTTACAGCTCTGATGGAACCTGCTGCCAATCAAGC	1740
DB	1681	AATTACTTGTGTCGCGCTTACAGCTCTGATGGAACCTGCTGCCAATCAAGC	1740
QY	1741	TTGASAMATCCCTTTGCGAGCTGGATACCAAAAGCCGACGAGCTTCCACAGTGCCA	1799
DB	1741	TTGASAMATCCCTTTGCGAGCTGGATACCAAAAGCCGACGAGCTTCCACAGTGCCA	1799

RESULT 3

US-09-370-265-2
; Sequence 2, Application US/09370265
; Patent No. 6447771
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28111/35908
; CURRENT APPLICATION NUMBER: US/09/370,265

CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: PCT/US99/16180
EARLIER FILING DATE: 1999-07-16
EARLIER APPLICATION NUMBER: 09/350,836
EARLIER FILING DATE: 1999-07-09
EARLIER APPLICATION NUMBER: 09/273,447
EARLIER FILING DATE: 1999-03-19
EARLIER APPLICATION NUMBER: 09/244,444
EARLIER FILING DATE: 1999-02-04
EARLIER APPLICATION NUMBER: 09/122,449
EARLIER FILING DATE: 1998-07-24
EARLIER APPLICATION NUMBER: 09/118,205
EARLIER FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 1799

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (246)..(1529)

FEATURE:

NAME/KEY: misc feature

LOCATION: (1718)

OTHER INFORMATION: n = adenine or guanine or thymine or cytosine or thymine

S-09-370-265-2

Query Match: 99.8%; Score 1794.8; DB 4; Length 1799;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y	1	CGCGGCTGCGCGCAAGGTGGCGCGCGCGCGCTTTCCTGTTCTCTGGTCAACAAAGAA	60
b	1	CGCGGCTGCGCGCAAGGTGGCGCGCGCGCGCTTTCCTGTTCTCTGGTCAACAAAGAA	60
y	61	TGTGGAGTGTCTTGGCTGAATCCTCATACAGACAAGATCAATATGGTGTCTAGGTGA	120
b	61	TGTGGAGTGTCTTGGCTGAATCCTCATACAGACAAGATCAATATGGTGTCTAGGTGA	120
y	121	AAAGTGAATTAATAAGGAACCAAGAGAAAATTCAGAAAGGAAGAAAATTTGCTCT	180
b	121	AAAGTGAATTAATAAGGAACCAAGAGAAAATTCAGAAAGGAAGAAAATTTGCTCT	180
y	181	GCAGGTGTGGAGCAGATGCTTCTGCAACAAAGCCTCCACGACGACCTTTGGGA	240
b	181	GCAGGTGTGGAGCAGATGCTTCTGCAACAAAGCCTCCACGACGACCTTTGGGA	240
y	241	AAAGATGGCCACTTCTTGGGGCACAGTCTTTTCAATGCTGTGGTATCTGTGTTGCA	300
b	241	AAAGATGGCCACTTCTTGGGGCACAGTCTTTTCAATGCTGTGGTATCTGTGTTGCA	300
y	301	CGCTGTCTCCACAGAAACAGCAGACTTGGTTGAGGATATCTTCTCTCTCCATGT	360
b	301	CGCTGTCTCCACAGAAACAGCAGACTTGGTTGAGGATATCTTCTCTCTCCATGT	360
y	361	GCCCATCAATGTCCAGCGCAGACCTTGTATGAAATATGTTGATGACGAGCAGCTG	420
b	361	GCCCATCAATGTCCAGCGCAGACCTTGTATGAAATATGTTGATGACGAGCAGCTG	420
y	421	GAATCGAATTCATSTTTACACCTTTTGTGAGAAAATGCCAGGACAGCTTCCAAATCTAG	480
b	421	GAATCGAATTCATSTTTACACCTTTTGTGAGAAAATGCCAGGACAGCTTCCAAATCTAG	480
y	481	AAGGGAGTTTGTATCTGTGAAGCAGACCTTCTGCTTTTGTAGATCAACCTAAGC	540
b	481	AAGGGAGTTTGTATCTGTGAAGCAGACCTTCTGCTTTTGTAGATCAACCTAAGC	540
y	541	AGGTGTGTAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGAAGTC	600
b	541	AGGTGTGTAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGAAGTC	600
y	601	ACTGAAAAAGACCCCAAGTGGTCTTAAAGGCAACAGCAGGACTACGTTACTCCAGAAC	660

Db	601	ACTGAAAAAGACCCCAAGTGGTCTTAAAGGCAACAGCAGGACTACGTTACTCCAGAAC	660
Qy	661	ACAAAGCCAAAGCTCTGCTCTTTGAGGTAAAGAGATCTTTCAGGAAGTCACTTTTCCTGG	720
Db	661	ACAAAGCCAAAGCTCTGCTCTTTGAGGTAAAGAGATCTTTCAGGAAGTCACTTTTCCTGG	720
Qy	721	TACCAAGGGCAGTGTAGCATCATGATCGATCCGAGGAAGGATATATAGCTTGGTTA	780
Db	721	TACCAAGGGCAGTGTAGCATCATGATCGATCCGAGGAAGGATATATAGCTTGGTTA	780
Qy	781	CTGTGAATTTTCTGACAGTGCAGTGCATGCCACAGACAGAGACTGTGGGGACCTTGG	840
Db	781	CTGTGAATTTTCTGACAGTGCAGTGCATGCCACAGACAGAGACTGTGGGGACCTTGG	840
Qy	841	ACCTAGGGGAGCCTCCACCCAAATCACGTTCTTCCGCCAGTTTGAAGAACTCTGGAAC	900
Db	841	ACCTAGGGGAGCCTCCACCCAAATCACGTTCTTCCGCCAGTTTGAAGAACTCTGGAAC	900
Qy	901	AAACTCTAGGGCTACTCTACTTCTTTGAGATGTTTACAGSACTTATAGCTCTATA	960
Db	901	AAACTCTAGGGCTACTCTACTTCTTTGAGATGTTTAAACAGCACTTAAAGCTCTATA	960
Qy	961	CACATAGTTACTCTGGATTTCGATTGAAAGCTGCAAGACTAGCAACCTCGGAGCCCTGG	1020
Db	961	CACATAGTTACTCTGGATTTCGATTGAAAGCTGCAAGACTAGCAACCTCGGAGCCCTGG	1020
Qy	1021	AGACAGAGGAGCTGATGGGCACACTTTCCGAGTGCCTGTTTACCAGATGTTTGAAG	1080
Db	1021	AGACAGAGGAGCTGATGGGCACACTTTCCGAGTGCCTGTTTACCAGATGTTTGAAG	1080
Qy	1081	CAGATGATCTTTGGGGTGTGAATACCAATACCAATATGTTGGCAACCAAGAGGAGGTGG	1140
Db	1081	CAGATGATCTTTGGGGTGTGAATACCAATACCAATATGTTGGCAACCAAGAGGAGGTGG	1140
Qy	1141	GCTTTGAGCCCTGCTATGCGCAAGTGTGAGGGTGTACAGAGGAAACTTCCACGAGCAG	1200
Db	1141	GCTTTGAGCCCTGCTATGCGCAAGTGTGAGGGTGTACAGAGGAAACTTCCACGAGCAG	1200
Qy	1201	AGGAGTCCAGAGAGTTCCTTCTATGCTTCTCTTACTATATGACCGAGCTGTGACA	1260
Db	1201	AGGAGTCCAGAGAGTTCCTTCTATGCTTCTCTTACTATATGACCGAGCTGTGACA	1260
Qy	1261	CAGATGATGATTATGAAGGGGGTATTTTAAAGTTGAAGTATTTGAAAGAAAG	1320
Db	1261	CAGATGATGATTATGAAGGGGGTATTTTAAAGTTGAAGTATTTGAAAGAAAG	1320
Qy	1321	CCAGGAAAGTGTGATAACTTGGAAAACTTCACTCAGGCAGTCTTCTCTGTGATGG	1380
Db	1321	CCAGGAAAGTGTGATAACTTGGAAAACTTCACTCAGGCAGTCTTCTCTGTGATGG	1380
Qy	1381	ATCTCAGCTACATCACAGCCCTGTAAAGGATGCTTGGCTTTGCAAGACAGCAGTCT	1440
Db	1381	ATCTCAGCTACATCACAGCCCTGTAAAGGATGCTTGGCTTTGCAAGACAGCAGTCT	1440
Qy	1441	TACAGCTCACAAAGAAAGTGAACATAGAGAGGGCTGGGCTTGGGGCCACCTTTC	1500
Db	1441	TACAGCTCACAAAGAAAGTGAACATAGAGAGGGCTGGGCTTGGGGCCACCTTTC	1500
Qy	1501	ACCTGTTGAGTCTCTGGGCATCTCCCATTCAGGCCAGCTTACTTCTTGGAGACCTGAT	1560
Db	1501	ACCTGTTGAGTCTCTGGGCATCTCCCATTCAGGCCAGCTTACTTCTTGGAGACCTGAT	1560
Qy	1561	TTGCCAACACCTTTTAAAGGGAGGAGAGACCTTAGTCTTCTGAACCTAGTCTGGGACA	1620
Db	1561	TTGCCAACACCTTTTAAAGGGAGGAGAGACCTTAGTCTTCTGAACCTAGTCTGGGACA	1620
Qy	1621	TCCTGAGCTCAGGCTTAGAGATTWRGTTAAATAACGCGCCGAGCTTATCTTATAGT	1680
Db	1621	TCCTGAGCTCAGGCTTAGAGATTWRGTTAAATAACGCGCCGAGCTTATCTTATAGT	1680
Qy	1681	AATTTACTTGTGCGCGCTTTACAGTCTGTGATGNNAAACCTGCGTCCCACTAAGC	1740
Db	1681	AATTTACTTGTGCGCGCTTTACAGTCTGTGATGNNAAACCTGCGTCCCACTAAGC	1740

1381 ATCTCAGCTACATCACAGCCCTGTTAAAGATGGCTTTGGCTTTGCGACAGACAGATCT 1440
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1381 ATCTCAGCTACATCACAGCCCTGTTAAAGATGGCTTTGGCTTTGCGACAGACAGATCT 1440
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1441 TACAGCTCAAAAGAAAGTGAACACATAGACAGCGCTGGCCCTTGGGGSCACCTTTC 1500
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1501 ACCTGTGAGCTCTGGCATCTCCATTAGGCCACGTACTTCTTTGGAGACCTGCAT 1560
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1501 ACCTGTGAGCTCTGGCATCTCCATTAGGCCACGTACTTCTTTGGAGACCTGCAT 1560
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1621 TCTGGACTTGAGCCCTAGAGATTWGTAAATTAASCGCGGAGCTTATCCTTWTATAGGT 1680
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1681 AATTACTTGCTGGCCGCTTTACACGTCGTGATGGNAACCTCGTCCCACTTAACGC 1740
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1741 TTGASMAATCCCTTCGAGCTCGCATACCAAGCGAGCGCTTCCACAGTGCCA 1799
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|||||

RESULT 5
5-09-240-639-5
Sequence 5, Application US/09240639
Patent No. 635047
GENERAL INFORMATION:
APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna-Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
FILE REFERENCE: 9598-066
CURRENT APPLICATION NUMBER: US/09/240,639
CURRENT FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (247)..(1530)
5-09-240-639-5

Query Match 87.5%; Score 1575; DB 4; Length 1998;
Best Local Similarity 98.2%; Pred. No. C;
Matches 1620; Conservative 2; Mismatches 2; Indels 25; Gaps 2;
24 GCGCGCGCTTTTCCTGCTCAACAAGAAATGTGGAGTGTCTTGCTGAATCC 63
1 GCGCGCGCTTTTCCTGCTCAACAAGAAATGTGGAGTGTCTTGCTGAATCC 60
84 TCATACAGACAGATCATTTATGCTGCTGTT-----AGGTG 119
61 TCATACAGACAGATCATTTATGCTGCTGTTAGTAGAGCTTGTATCCAGATGTAAGGTG 120
120 AAAAGTGATATAAATAAGAAACCAAGGAGAAAATTCAGAAAGAAAGAAAATTCGCTC 179
121 AAAAGTGATATAAATAAGAAACCAAGGAGAAAATTCAGAAAGAAAGAAAATTCGCTC 180
180 TCGAGTGTGCGAGAGGATTCGCTTCGCAACAAAGCGCTCCACCAGCACATCTTGGG 239
181 TCGAGTGTGCGAGAGGATTCGCTTCGCAACAAAGCGCTCCACCAGCACATCTTGGG 240

QY 240 AAAAGATGGCACTTCTTTGGGCAAGTCTTTTTCATGCTGTGTGTATCTGTGTTC 299
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QY 241 AAAAGATGGCACTTCTTTGGGCAAGTCTTTTTCATGCTGTGTGTATCTGTGTTC 300
DB |||||
QY 300 AGCGTGTCTCCACAGGAACACAGACACTGGTTTGGAGGTAATCTTCTGTCTTCCATG 359
DB |||||
QY 301 AGCGTGTCTCCACAGGAACACAGACACTGGTTTGGAGGTAATCTTCTGTCTTCCATG 360
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QY 360 TGCCCATCAATGTACGCGCCAGCACTTTGTATGGAATATATGTTTATGACGAGGACACT 419
DB |||||
QY 361 TGCCCATCAATGTACGCGCCAGCACTTTGTATGGAATATATGTTTATGACGAGGACACT 420
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QY 420 GGAATCTGAATTCATGTTTACACCTTTGTGCAAGAAATSCCAGGACAGCTTCCAATCTA 479
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QY 421 GGAATCTGAATTCATGTTTACACCTTTGTGCAAGAAATSCCAGGACAGCTTCCAATCTA 480
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QY 480 GGAAGGGAAGCTTTTTCATCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAG 539
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QY 481 GGAAGGGAAGCTTTTTCATCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACCTAAG 540
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QY 600 CACTGGAAGAACCCAGTGTCTTAAGGCTCTTAAGGCTGGCCAAAGACTCAATCCCCGAACT 659
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QY 601 CACTGGAAGAACCCAGTGTCTTAAGGCTCTTAAGGCTGGCCAAAGACTCAATCCCCGAACT 660
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QY 660 CACAAGCCAAAGCTCTGCTTTTGAAGTAAAGGAGACTCTTCAAGGAAGTCACTTTTCTG 719
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QY 661 CACAAGCCAAAGCTCTGCTTTTGAAGTAAAGGAGACTCTTCAAGGAAGTCACTTTTCTG 720
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QY 720 GTACCAAGGGCAGTGTAGCATCATGGATGGATCCGCAAGGCATATAGCTTGGGT 779
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QY 721 GTACCAAGGGCAGTGTAGCATCATGGATGGATCCGCAAGGCATATAGCTTGGGT 780
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QY 780 ACTGTGAATTTCTGACAGCTGAGCTGCATGGCCACAGACAGGAGACTGTGGGACCTTG 839
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QY 781 ACTGTGAATTTCTGACAGCTGAGCTGCATGGCCACAGACAGGAGACTGTGGGACCTTG 840
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QY 840 GACTAGGGGGAGCTCCACCCAAATCAGCTTCTGCCCCCAGTTTGAAGAACTCTGGA 899
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QY 841 GACTAGGGGGAGCTCCACCCAAATCAGCTTCTGCCCCCAGTTTGAAGAACTCTGGA 900
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QY 900 CAAACTCTAGGGGCTACCTCACTTCTGAGATCTTTAAAGACACTTATAGCTCTAT 959
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QY 901 CAAACTCTAGGGGCTACCTCACTTCTGAGATCTTTAAAGACACTTATAGCTCTAT 960
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QY 960 ACACATAGTTTACCTGGGATTTGGATTTGAAGCTGCAAGACTAGCAACCTGGAGGCCCTG 1019
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QY 961 ACACATAGTTTACCTGGGATTTGGATTTGAAGCTGCAAGACTAGCAACCTGGAGGCCCTG 1020
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QY 1020 GAGACAGAGGACTCATGGGCACTTTCCGAGTGCCTTTTACCAGATGTTTGGAA 1079
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QY 1021 GAGACAGAGGACTCATGGGCACTTTCCGAGTGCCTTTTACCAGATGTTTGGAA 1080
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QY 1080 GCGAGTGGATCTTTGGGGGTGGAATACCATATGTTGGGCAACCAAGAGGGGAGGTG 1139
DB |||||
QY 1081 GCGAGTGGATCTTTGGGGGTGGAATACCATATGTTGGGCAACCAAGAGGGGAGGTG 1140
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QY 1140 GCGTGTGAGCCCTGCTATGCCGAAGTCTGAGGCTGTTACGAGAAACTTACACAGCCA 1199
DB |||||
QY 1141 GCGTGTGAGCCCTGCTATGCCGAAGTCTGAGGCTGTTACGAGAAACTTACACAGCCA 1200
DB |||||
QY 1200 GAGGAGGTCCAGAGAGGTTCTTCTATGCTTTCTTTACTATTTATGACCGAGCTGTGAC 1259
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QY 1201 GAGGAGGTCCAGAGAGGTTCTTCTATGCTTTCTTTACTATTTATGACCGAGCTGTGAC 1260
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QY 1260 ACAGACATGTTGATTTAAGAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAA 1319
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QY 1261 ACAGACATGTTGATTTAAGAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAA 1320
DB |||||
QY 1320 GCCAGGAGTGTGTGATTAACCTTGGAAAACTTCACTCAGGAGTCTTCTTCTGTGTCATG 1379

||||| 1321 GCAGGGAAGTGTGATAAATGGAAATCTCACTCAGGCAAGTCTTCTGTGTCATG 1390
||||| 1380 GATCTCAGCTACATCACAGCCCTGTTAAAGGATGCTTTGGCTTTGACAGACAGACAGTC 1439
||||| 1381 GATCTCAGCTACATCACAGCCCTGTTAAAGGATGCTTTGGCTTTGACAGACAGACAGTC 1440
||||| 1440 TTACAGCTCACAAAGAAAGTGAACACATAGACAGCGGCTGGGCTTTGGGGCCACCTTT 1499
||||| 1441 TTACAGCTCACAAAGAAAGTGAACACATAGACAGCGGCTGGGCTTTGGGGCCACCTTT 1500
||||| 1500 CACCTGTTGCACTCTCTGGGCAATCTCCCATGAGCCAGGTAATCTTCTTGGAGACTGCA 1559
||||| 1501 CACCTGTTGCACTCTCTGGGCAATCTCCCATGAGCCAGGTAATCTTCTTGGAGACTGCA 1560
||||| 1560 TTGCGCAACACCTTTTAAAGGGAGGAGAGACACTTACTTCTGAACTAGTCTTGGGAC 1619
||||| 1561 TTGCGCAACACCTTTTAAAGGGAGGAGAGACACTTACTTCTGAACTAGTCTTGGGAC 1620
||||| 1620 ATCTGGACTTGAGCTTAGAGATTWRTT 1648
||||| 1620 ATCTGGACTTGAGCTTAGAGATTWRTT 1648

RESULT 6

S-09-608-285A-24
Sequence 24, Application US/09608285A
Patent No. 6335013

GENERAL INFORMATION:

APPLICANT: Ford, John
APPLICANT: Melero, Julio
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/36570

CURRENT APPLICATION NUMBER: JS/09/608, 285A

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: 09/583,231

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 09/557,800

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 09/481,238

PRIOR FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: 09/370,265

PRIOR FILING DATE: 1999-08-09

PRIOR APPLICATION NUMBER: PCT/US99/16180

PRIOR FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: 09/350,836

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: 09/273,447

PRIOR FILING DATE: 1999-03-19

PRIOR APPLICATION NUMBER: 09/244,444

PRIOR FILING DATE: 1999-02-04

PRIOR APPLICATION NUMBER: 09/122,449

PRIOR FILING DATE: 1998-07-24

PRIOR APPLICATION NUMBER: 09/118,205

PRIOR FILING DATE: 1998-07-16

NUMBER OF SEQ ID NOS: 60

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 24

LENGTH: 1601

TYPE: DNA

ORGANISM: Homo sapiens

S-09-608-285A-24

Query Match 80.3%; Score 1445; DB 4; Length 1601;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCGGGCTGCGCGCAAGGGTGGCGCGCGCGGCTTTCTCTGTTCTCTGGTCAACAAGAAA 60

1 GCGGGCTGCGCGCAAGGGTGGCGCGCGCGGCTTTCTCTGTTCTCTGGTCAACAAGAAA 60

QY 61 TGTGGAGTGTCTGGCTGAATCCTCTACACAGACAAGATCATTTATGGTGTCTGTTAGGTTGA 120
DB 61 TGTGGAGTGTCTGGCTGAATCCTCTACACAGACAAGATCATTTATGGTGTCTGTTAGGTTGA 120
QY 121 AAAAGTCATATAATAAGGAACCAAGGAGAAATTCAGAAGGAAAGAAATAATTCGCTCT 180
DB 121 AAAAGTCATATAATAAGGAACCAAGGAGAAATTCAGAAGGAAAGAAATAATTCGCTCT 180
QY 181 GCAGGTGTGGAGCAGGATTTCTTTCGAACAAGGCTCCACCCAGCCACATCTTCGGGA 240
DB 181 GCAGGTGTGGAGCAGGATTTCTTTCGAACAAGGCTCCACCCAGCCACATCTTCGGGA 240
QY 241 AAAGATGGCCACTTCTTGGGGCACAGTCTTTTCATGCTGGTGGTATCTGTGTTTGA 300
DB 241 AAAGATGGCCACTTCTTGGGGCACAGTCTTTTCATGCTGGTGGTATCTGTGTTTGA 300
QY 301 GCGCTGTCTCCACAGGAACACAGACACTTGGTTTGAAGGTATCTTCTCTCTTCATGT 360
DB 301 GCGCTGTCTCCACAGGAACACAGACACTTGGTTTGAAGGTATCTTCTCTCTTCATGT 360
QY 361 GCCCATCAATGTGAGCCGACACCTTTGTATGSAATTTATTTGATGAGGAGCACTG 420
DB 361 GCCCATCAATGTGAGCCGACACCTTTGTATGSAATTTATTTGATGAGGAGCACTG 420
QY 421 GAATCGAATTCATGTTTACACCTTTGTGAGGAAATGCCAGGACAGCTTCCAATTCAG 480
DB 421 GAATCGAATTCATGTTTACACCTTTGTGAGGAAATGCCAGGACAGCTTCCAATTCAG 480
QY 481 AAGCGGAAGTTTGTGTTGAGGAGGAGGAGTCTTCTGCTTTTGTAGATCAACTAAGC 540
DB 481 AAGCGGAAGTTTGTGTTGAGGAGGAGGAGTCTTCTGCTTTTGTAGATCAACTAAGC 540
QY 541 AGGTGTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCGGAAGTC 600
DB 541 AGGTGTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCGGAAGTC 600
QY 601 ACTGGAAGGAGCCCGAGTGGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCGAAGC 660
DB 601 ACTGGAAGGAGCCCGAGTGGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCGAAGC 660
QY 661 ACAAGCCAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAGGAAGTCACCTTTCTCGG 720
DB 661 ACAAGCCAGGCTCTGCTCTTTGAGGTAAAGGAGATCTTCAGGAAGTCACCTTTCTCGG 720
QY 721 TACCAAGGCGCAGTGTTAGCATCATGATGATCCGACGAAGGCATATTAGCTTGGTGA 780
DB 721 TACCAAGGCGCAGTGTTAGCATCATGATGATCCGACGAAGGCATATTAGCTTGGTGA 780
QY 781 CTGTGAATTTTCTGACAGGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 840
DB 781 CTGTGAATTTTCTGACAGGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 840
QY 841 ACCTAGGGGAGCCTCCACCCAAATCAGTTCCTGCCCCAGTTTGGAGAACTCTGGAAC 900
DB 841 ACCTAGGGGAGCCTCCACCCAAATCAGTTCCTGCCCCAGTTTGGAGAACTCTGGAAC 900
QY 901 AAATCTCTAGGGGTACCTCACTCTCTTTGAGATGTTTAAAGCAGCACTTATAAGCTCTATA 960
DB 901 AAATCTCTAGGGGTACCTCACTCTCTTTGAGATGTTTAAAGCAGCACTTATAAGCTCTATA 960
QY 961 CACATAGTTTACCTGGGATTTGGATTTGAAAGCTGCAAGACTAGCAACCTGGGAGCCCTGG 1020
DB 961 CACATAGTTTACCTGGGATTTGGATTTGAAAGCTGCAAGACTAGCAACCTGGGAGCCCTGG 1020
QY 1021 AGCAGAGGAGGACTGATGGGACACTTTTCGGGAGTGGCTGTTTACCAGATGTTTGAAG 1080
DB 1021 AGCAGAGGAGGACTGATGGGACACTTTTCGGGAGTGGCTGTTTACCAGATGTTTGAAG 1080
QY 1081 CAGAGTGGATCTTTGGGGGTGTGAAATACCAAGTATGGTGGCAACCAAGAGGGGAGGTGG 1140
DB 1081 CAGAGTGGATCTTTGGGGGTGTGAAATACCAAGTATGGTGGCAACCAAGAGGGGAGGTGG 1140
QY 1141 GCTTTGAGCCCTGCTATGCGCGAAGTGTGAGGGTGTGACGAGGAAATCTTACCAGCCAG 1200

1261 CAGACATGATTGATTATGAAAGGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAG 1320
1321 CCAGGAAGTGTGTGATAACTTGGAAAACTTCACCTCAGGCAGTCTTTCTCTGTGCATGG 1380
1321 CCAGGAAGTGTGTGATAACTTGGAAAACTTCACCTCAGGCAGTCTTTCTCTGTGCATGG 1380
1381 ATCTCAGCTACATCAGAGCCCTGTTAAAGATGAGCTTTGGCTTTGAGACACACAGTCT 1440
1381 ATCTCAGCTACATCAGAGCCCTGTTAAAGATGAGCTTTGGCTTTGAGACACACAGTCT 1440
1441 TACAG 1445
1441 TACAG 1445

RESULT 8
S-09-557-800C-24
Sequence 24, Application US/09557800C
Patent No.: 6476211
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 28110/36457
CURRENT APPLICATION NUMBER: US/09/557,800C
CURRENT FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/122449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/244444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 24
LENGTH: 1601
TYPE: DNA
ORGANISM: Homo sapiens

Query Match 80.3%; Score 1445; DB 4; Length 1601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCGGCTGCGCGCAAGGTGGCGCGCGCTTTCTTTCTCTGTGTCACAAAGAAA 60
1 GCGGCTGCGCGCAAGGTGGCGCGCGCTTTCTTTCTCTGTGTCACAAAGAAA 60
61 TGTGGAGTGTCTTGGCTGAATCTCTATACAGACAGATCATTTATGGTGTCTGTAGTTGA 120
61 TGTGGAGTGTCTTGGCTGAATCTCTATACAGACAGATCATTTATGGTGTCTGTAGTTGA 120
121 AAAAGTGATATATAAGGACCAAGGAGAAATTCAGAGGAAAGAAAATTCCTCT 180
121 AAAAGTGATATATAAGGACCAAGGAGAAATTCAGAGGAAAGAAAATTCCTCT 180
181 GCAGGTGTGGAGCAGGATGTCTTCTGCAACAAAGCCCTCCACCCAGGCACATCTGGGA 240
181 GCAGGTGTGGAGCAGGATGTCTTCTGCAACAAAGCCCTCCACCCAGGCACATCTGGGA 240
241 AAAGAAATGCCCATCTCTTGGGACAGCTCTTTTTCATGTCTGTGTATCTCTGTGTTGCA 300

241 AAAGAAATGCCCATCTCTTGGGACAGCTCTTTTCAAGCTGGTGTATCTCTGTGTTGCA 300
301 GCGCTGTCTCCACAGGACCAAGCAGACTTGGTTTGGAGGTATCTTCTCTCTCCATGT 360
301 GCGCTGTCTCCACAGGACCAAGCAGACTTGGTTTGGAGGTATCTTCTCTCTCCATGT 360
361 GCCCATCAATGTCTCAGGCCAGCAGCTTGTATGAATATGTTTGTGATGAGGAGCAGT 420
361 GCCCATCAATGTCTCAGGCCAGCAGCTTGTATGAATATGTTTGTGATGAGGAGCAGT 420
421 GAATCGAATTCATGTCTTACACCTTTGTGAGAAAAATGCCAGGACAGCTTCCAAATCTAG 480
421 GAATCGAATTCATGTCTTACACCTTTGTGAGAAAAATGCCAGGACAGCTTCCAAATCTAG 480
481 AAGGGGAAGTTTGAATCTGTGGAAGCCAGACTTCTGCTTTGTAGATCAACTAAGC 540
481 AAGGGGAAGTTTGAATCTGTGGAAGCCAGACTTCTGCTTTGTAGATCAACTAAGC 540
541 AGGTGTCTGAGACCGTTCAAGGGCTCTTAAAGGCAAGCAGGAGTCTCAATCCCGGAAATC 600
541 AGGTGTCTGAGACCGTTCAAGGGCTCTTAAAGGCAAGCAGGAGTCTCAATCCCGGAAATC 600
601 ACTGAAAAAGACCCAGTGTCTTAAAGGCAAGCAGGAGTCTCAATCCCGGAAATC 660
601 ACTGAAAAAGACCCAGTGTCTTAAAGGCAAGCAGGAGTCTCAATCCCGGAAATC 660
661 ACAAGCAAGCTCTCTCTTCAAGGTAAGGAGATCTTCAAGGAGTCTCAATCCCGGAAATC 720
661 ACAAGCAAGCTCTCTCTTCAAGGTAAGGAGATCTTCAAGGAGTCTCAATCCCGGAAATC 720
721 TACCAAGGCAAGTGTAGCATATGATGATCCGACGAGGATATTAAGCTTSGGTTA 780
721 TACCAAGGCAAGTGTAGCATATGATGATCCGACGAGGATATTAAGCTTSGGTTA 780
781 CTGTGAATTTCTGACAGGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 840
781 CTGTGAATTTCTGACAGGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 840
841 ACCTAGGGGAGCTCTCCACCAATCAGCTTCTGCGCCCGAGTTTGAGAAACTCTGGAAC 900
841 ACCTAGGGGAGCTCTCCACCAATCAGCTTCTGCGCCCGAGTTTGAGAAACTCTGGAAC 900
901 AAATCTCTAGGGGCTAGCTCACTTCTCTTCTGAGATGTTTAAAGCACTTATTAAGCTCTATA 960
901 AAATCTCTAGGGGCTAGCTCACTTCTCTTCTGAGATGTTTAAAGCACTTATTAAGCTCTATA 960
961 CACATAGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTGGAGCCCTGG 1020
961 CACATAGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTGGAGCCCTGG 1020
1021 AGCAGAGGAGCTGATGGGCACACTTTCCGGAGTGGCTGTTTACCCAGATGTTTGGAG 1080
1021 AGCAGAGGAGCTGATGGGCACACTTTCCGGAGTGGCTGTTTACCCAGATGTTTGGAG 1080
1081 CAGAGTGGATCTTTGGGGGTGTGAATACCAAGTATGTTGSCAACCAAGAGGGGAGGTGG 1140
1081 CAGAGTGGATCTTTGGGGGTGTGAATACCAAGTATGTTGSCAACCAAGAGGGGAGGTGG 1140
1141 GCTTTGAGCCCTGCTATGCCGAAGTGTGAGGTGGTACGAGGAAATCTTCAACAGCCAG 1200
1141 GCTTTGAGCCCTGCTATGCCGAAGTGTGAGGTGGTACGAGGAAATCTTCAACAGCCAG 1200
1201 AGGAGGTCCAGAGAGGTCTCTCTATCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1260
1201 AGGAGGTCCAGAGAGGTCTCTCTATCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1260
1261 CAGACATGATTTGATTTGAAAGGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAAG 1320
1261 CAGACATGATTTGATTTGAAAGGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAAG 1320
1321 CCAGGAAGTGTGTGATAACTTGGAAAACTTCACCTCAGGCAGTCTTTCTCTGTGCATGG 1380

RESULT 10
S-09-350-836B-4
Sequence 4, Application US/09350836B
Patent No. 6387645
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
FILE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/35161
CURRENT APPLICATION NUMBER: US/09/350,836B
CURRENT FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1287
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1284)
S-09-350-836B-4
Query Match 71.5%; Score 1287; DB 4; Length 1287;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 246 ATGGCCACTTCTGGGGCCACAGTCCTTTTTCATGCTGGTGGTATCCCTGGTTTGCAGCGCT 305
D 1 ATGGCCACTTCTGGGGCCACAGTCCTTTTTCATGCTGGTGGTATCCCTGGTTTGCAGCGCT 60
Y 306 GTCCTCCACAGAACACAGACACTGGTTTGGAGGTATCTCTGCTCCATGTCAGCGCT 365
D 61 GTCCTCCACAGAACACAGACACTGGTTTGGAGGTATCTCTGCTCCATGTCAGCGCT 120
Y 366 ATCAATGTGAGCGCCAGCACCTTGTATGGAATTATGTTGATGAGGAGGACACTGGAAC 425
D 121 ATCAATGTGAGCGCCAGCACCTTGTATGGAATTATGTTGATGAGGAGGACACTGGAAC 180
Y 426 CGAATTCATGTTTACACCTTTGTGAGAGAAAAGCCAGGACAGCTTCCAAATCTAGAAAGG 485
D 181 CGAATTCATGTTTACACCTTTGTGAGAGAAAAGCCAGGACAGCTTCCAAATCTAGAAAGG 240
Y 486 GAAGTTTTCATCTGTGAAGCCAGACACTTCTGCTTGTAGATCACTTAAGCAGGCT 545
D 241 GAAGTTTTCATCTGTGAAGCCAGACACTTCTGCTTGTAGATCACTTAAGCAGGCT 300
Y 546 GCTGAGACCGTTCAAGGCTCTTAGAGTGGCCAAAGACTCAATCCCGGAAGTCACTGG 605
D 301 GCTGAGACCGTTCAAGGCTCTTAGAGTGGCCAAAGACTCAATCCCGGAAGTCACTGG 360
Y 606 AAAAGACCCAGTGGTCTTAAAGCAACAGGAGGACTACGTTTACTGCGAAGACACAAA 665
D 361 AAAAGACCCAGTGGTCTTAAAGCAACAGGAGGACTACGTTTACTGCGAAGACACAAA 420
Y 666 GGCNAGGCTGCTCTTTCAGGTAAAGGAGATCTTCAGGAAGTCACTTTCCTGTGACCA 725
D 421 GGCNAGGCTGCTCTTTCAGGTAAAGGAGATCTTCAGGAAGTCACTTTCCTGTGACCA 480
Y 726 AAGGGCAGTGTAGCATCATGATGATCCGACGAGGACATATTAGCTTGGGTTACTGTG 785
D 481 AAGGGCAGTGTAGCATCATGATGATCCGACGAGGACATATTAGCTTGGGTTACTGTG 540

QY 786 AATTTTCTGACAGGTGACCTGACATGGCCACAGACAGAGACTGTGGGACCTTGGACCTA 845
DB |||||
541 AATTTTCTGACAGGTGACCTGACATGGCCACAGACAGAGACTGTGGGACCTTGGACCTA 600
QY 846 GGGGAGGCTCCACCCAAATCACGTTCTCTGCCAGTTTGAGAAAACTCTGGAAACAACT 905
DB |||||
601 GGGGAGGCTCCACCCAAATCACGTTCTCTGCCAGTTTGAGAAAACTCTGGAAACAACT 660
QY 906 CTTAGGGCTACCTCACTTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACACAT 965
DB |||||
661 CTTAGGGCTACCTCACTTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACACAT 720
QY 966 AGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAAACTTCCAGGAGGCTTGGAGACA 1025
DB |||||
721 AGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAAACTTCCAGGAGGCTTGGAGACA 780
QY 1026 GAAGGAGCTGATGGGACACCTTCCGGAGTGCCTTTTACCGAGATGTTTGGAGACAGAG 1085
DB |||||
781 GAAGGAGCTGATGGGACACCTTCCGGAGTGCCTTTTACCGAGATGTTTGGAGACAGAG 840
QY 1086 TGGATCTTTGGGGGTGTCAAATACCAATACCAATACCAATACCAATACCAATACCAATACCAAT 1145
DB |||||
841 TGGATCTTTGGGGGTGTCAAATACCAATACCAATACCAATACCAATACCAATACCAATACCAAT 900
QY 1146 GAGCCCTGCTATGCCGAAGTCTGAGGGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1205
DB |||||
901 GAGCCCTGCTATGCCGAAGTCTGAGGGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
QY 1206 GTCCAGAGAGGTTCTTCTATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1265
DB |||||
961 GTCCAGAGAGGTTCTTCTATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1020
QY 1266 ATGATTGATTATGAAAGGGGGGTATTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTT 1325
DB |||||
1021 ATGATTGATTATGAAAGGGGGGTATTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAAAGTT 1080
QY 1326 GAAGTGTGATTAACCTTGGAAACTTCACTCAGGAGTCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCT 1385
DB |||||
1081 GAAGTGTGATTAACCTTGGAAACTTCACTCAGGAGTCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1386 AGCTACATCACAGCCCTGTTAAAGGATGGCTTGGCTTTCGAGACAGACAGACAGCTTACAG 1445
DB |||||
1441 AGCTACATCACAGCCCTGTTAAAGGATGGCTTGGCTTTCGAGACAGACAGACAGCTTACAG 1200
QY 1446 CTCACAAAGAAAGTGAACACATAGACGCGCTGGGCTTGGGCGCCACCTTTTCACCTG 1505
DB |||||
1201 CTCACAAAGAAAGTGAACACATAGACGCGCTGGGCTTGGGCGCCACCTTTTCACCTG 1260
QY 1506 TTGAGTCTCTGGGCTCTCCCATTTGA 1532
DB |||||
1261 TTGAGTCTCTGGGCTCTCCCATTTGA 1287

RESULT 11
US-09-370-265-4
Sequence 4, Application US/09370265
Patent No. 6447771
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
FILE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28111/35908
CURRENT APPLICATION NUMBER: US/09/370,265
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: PCT/US99/16180
EARLIER FILING DATE: 1999-07-16
EARLIER APPLICATION NUMBER: 09/350,836
EARLIER FILING DATE: 1999-07-09
EARLIER APPLICATION NUMBER: 09/273,447
EARLIER FILING DATE: 1999-03-19
EARLIER APPLICATION NUMBER: 09/244,444
EARLIER FILING DATE: 1999-02-04

5-09-557-800C-4

Query Match 71.5%; Score 1287; DB 4; Length 1287;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

246 ATGGCCACTTCTGGGGCAGCAGCTTTTTCATGCTGGTGGTATCTGTGTTTGCAGCGCT 305
1 ATGGCCACTTCTGGGGCAGCAGCTTTTTCATGCTGGTGGTATCTGTGTTTGCAGCGCT 60

306 GTCTCCACAGAACCCAGCAGACTTTGGTTGAGGGTATCTTCTCTCTTCCATGTCGCC 365
61 GTCTCCACAGAACCCAGCAGACTTTGGTTGAGGGTATCTTCTCTCTTCCATGTCGCC 120

366 ATCAATGTACGCCAGCAGCAGCTTTGATGGAATTAATGTTGATGAGGAGCAGCTGGAAT 425
121 ATCAATGTACGCCAGCAGCAGCTTTGATGGAATTAATGTTGATGAGGAGCAGCTGGAAT 180

426 CGAATTCATGTTTACACCTTTGTCGAGAAATGCCAGGACAGCTTCCAAATCTAGAGGG 485
181 CGAATTCATGTTTACACCTTTGTCGAGAAATGCCAGGACAGCTTCCAAATCTAGAGGG 240

486 GAAATGTTTGAATCTGTGAAGCAGGAGCTTTCTGCTTTTGTAGATCAACCTAAGCAGGGT 545
241 GAAATGTTTGAATCTGTGAAGCAGGAGCTTTCTGCTTTTGTAGATCAACCTAAGCAGGGT 300

546 GCTGAGACCGTTCAAGGGCTCTTAGAGTGGCCAAAGACTCAATCCCGCAGTCACTGG 605
301 GCTGAGACCGTTCAAGGGCTCTTAGAGTGGCCAAAGACTCAATCCCGCAGTCACTGG 360

606 AAAAGAGCCCAAGTGGTCTTAAGGCAACAGCAGACTTACTGCCAGACACAAA 665
361 AAAAGAGCCCAAGTGGTCTTAAGGCAACAGCAGACTTACTGCCAGACACAAA 420

666 GCAAGGCTCTGCTCTTTGAGTAAAGGAGATCTTCAGGAAGTCACTTCTGCTGATCA 725
421 GCAAGGCTCTGCTCTTTGAGTAAAGGAGATCTTCAGGAAGTCACTTCTGCTGATCA 480

726 AAGGCGAGTGTAGCATCATGATGATCCGACGAGGCAATATAGCTTGGGTACTGTG 785
481 AAGGCGAGTGTAGCATCATGATGATCCGACGAGGCAATATAGCTTGGGTACTGTG 540

786 AATTTCTGACAGGTCAGCTGATGCCACACAGGAGACTGTGGGACCTTGGACCTA 845
541 AATTTCTGACAGGTCAGCTGATGCCACACAGGAGACTGTGGGACCTTGGACCTA 600

846 GGGGAGGCTCCACCAAAATCACTGTTCTGCCCCAGTTTGAGAAAATCTGGAACAACT 905
601 GGGGAGGCTCCACCAAAATCACTGTTCTGCCCCAGTTTGAGAAAATCTGGAACAACT 660

906 CTTAGGGGCTACTCACTTCTCTTGGATGTTTAAACAGACTTATAAGCTTATACAT 965
661 CTTAGGGGCTACTCACTTCTCTTGGATGTTTAAACAGACTTATAAGCTTATACAT 720

966 AGTTACCTGGGATTTGGATTGAAGCTCGAGACTAGCAACCTGGGAGCCTGGAGACA 1025
721 AGTTACCTGGGATTTGGATTGAAGCTCGAGACTAGCAACCTGGGAGCCTGGAGACA 780

1026 GAAAGGACTGATGGGCACACTTTCCGGAGTGCCTGTTTACCAGATGGTTGGAACGACAG 1085
781 GAAAGGACTGATGGGCACACTTTCCGGAGTGCCTGTTTACCAGATGGTTGGAACGACAG 840

1086 TGGATCTTTGGGGGTGTGAATAACAGTATGTTGGCAACCAAGAGAGGAGGTGGGCTTT 1145
841 TGGATCTTTGGGGGTGTGAATAACAGTATGTTGGCAACCAAGAGAGGAGGTGGGCTTT 900

1146 GAGCCCTGCTATGCCGAGTGTGAGGGTGTACAGGAGAAATCTTACAGCCAGGAGAG 1205
901 GAGCCCTGCTATGCCGAGTGTGAGGGTGTACAGGAGAAATCTTACAGCCAGGAGAG 960

1206 GTCCAGAGAGGTTCTCTTCTACTTCTCTTACTATATGACCGAGCTGTTGACACAC 1265
961 GTCCAGAGAGGTTCTCTTCTACTTCTCTTACTATATGACCGAGCTGTTGACACAC 1020

Qy 1266 ATGATTGATTATGAAAAGGGGGGTATTTTAAAGTTTGAAGATTTTGAAAGAAAGCCAGG 1325
Db 1021 ATGATTGATTATGAAAAGGGGGGTATTTTAAAGTTTGAAGATTTTGAAAGAAAGCCAGG 1080

Qy 1326 GAAGTGTGTGATTAACCTTGGAAAACCTTCACTCAGGAGTCTCTTCTCTGTGATGGATCTC 1385
Db 1081 GAAGTGTGTGATTAACCTTGGAAAACCTTCACTCAGGAGTCTCTTCTCTGTGATGGATCTC 1140

Qy 1386 AGCTACATCACAGCCCTGTTTAAAGGATGGCTTTTGGCTTTGCAGACAGCAGCTTTACAG 1445
Db 1141 AGCTACATCACAGCCCTGTTTAAAGGATGGCTTTTGGCTTTGCAGACAGCAGCTTTACAG 1200

Qy 1446 CTCACAAAGAAAGTGAACAACATAGACAGGGCTGGGCCCTTGGGGGCCACCTTTCACTG 1505
Db 1201 CTCACAAAGAAAGTGAACAACATAGACAGGGCTGGGCCCTTGGGGGCCACCTTTCACTG 1260

Qy 1506 TTGCAGTCTCTGGGCATCTCCCATTTGA 1532
Db 1261 TTGCAGTCTCTGGGCATCTCCCATTTGA 1287

RESULT 13
US-09-608-285A-6
; Sequence 6, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn, Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1284)
US-09-608-285A-6

Query Match 71.0%; Score 1277.4; DB 4; Length 1287;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1281; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 246 ATGGCCACTTCTGGGGCAGCAGCTTTTTCATGCTGGTGGTATCTCTGTGTTTGCAGCGCT 305
Db 1 ATGGCCACTTCTTGGGGCAGCAGCTTTTTCATGCTGGTGGTATCTCTGTGTTTGCAGCGCT 60

306 GTCTCCACAGGACCAGACAGACTTGGTTTGGGGTATCTTCTGCTCTCCATGTGCCCC 365
61 GTCTCCACAGGACCAGACAGACTTGGTTTGGGGTATCTTCTGCTCTCCATGTGCCCC 120
366 ATCAATGTTCAGGCCAGCAGCCTTGTATGAAATTATGTTTGTATGTCAGGGAGCAGCTTGAAGT 425
121 ATCAATGTTCAGGCCAGCAGCCTTGTATGAAATTATGTTTGTATGTCAGGGAGCAGCTTGAAGT 180
426 CGAATTCATGTTTACACCTTTGTSCAGAAATGCCAGACAGCTTCCCAATTTAGAAAGG 485
181 CGAATTCATGTTTACACCTTTGTSCAGAAATGCCAGACAGCTTCCCAATTTAGAAAGG 240
486 GAAGTTTTCATGTTTACACCTTTGTSCAGACAGCTTCCCAATTTAGAAAGG 545
241 GAAGTTTTCATGTTTACACCTTTGTSCAGACAGCTTCCCAATTTAGAAAGG 300
546 GCTGAGACCTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGAAAGTCACTGG 605
301 GCTGAGACCTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGAAAGTCACTGG 360
606 AAAAAAGCCCCAGTGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAACACAA 665
361 AAAAAAGCCCCAGTGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAACACAA 420
666 SCCAAGGCTCTGCTCTTGAAGGTAAAGGAGACTCTTCAGGAGTCACTTTCCTGCTACCA 725
421 SCCAAGGCTCTGCTCTTGAAGGTAAAGGAGACTCTTCAGGAGTCACTTTCCTGCTACCA 480
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481 AAGGCGAGTGTAGCATCATGATGATCCGAAAGGATATTAAGCTTGGGTTACTGTG 540
786 AATTTCTGACAGGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 845
541 AATTTCTGACAGGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
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966 AGTACCTGGGATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1025
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; Sequence 6, Application US/09350836B
; Patent No. 6387645
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/09/350.836B
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1284)
US-09-350-836B-6
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Best Local Similarity 99.58; Pred. No. 0;
Matches 1281; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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721 AGTTACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCTGGGAGCCCTGGAGACA 780
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781 GAAGGACACTGATGGGCACACTTTCCGAGTGCCTGTTTACCGAGATGGTGGAAAGCAGAG 840
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total number of hits satisfying chosen parameters: 3416838

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Maximum Match: 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	1794.8	99.8	1799	12	US-10-286-926-2
2	1794.8	99.8	1799	13	US-10-091-085-2
3	1794.8	99.8	1799	13	US-10-092-063-2
4	1445	80.3	1601	12	US-10-286-926-24
5	1445	80.3	1601	13	US-10-092-063-24
6	1287	71.5	1287	12	US-10-286-926-4
7	1287	71.5	1287	13	US-10-091-085-4
8	1287	71.5	1287	13	US-10-092-063-4
9	1277.4	71.0	1287	12	US-10-286-926-6
10	1277.4	71.0	1287	13	US-10-091-085-6
11	1277.4	71.0	1287	13	US-10-092-063-6
12	1089.2	60.5	1457	9	US-09-925-299-103
13	1089.2	60.5	1457	11	US-09-925-299-103
14	476	26.5	978	14	US-10-198-846-12729
15	359.2	20.0	420	10	US-09-960-352-11752
16	342.2	19.0	2693	12	US-10-286-926-48

Sequence 26, Appl
Sequence 52, Appl
Sequence 26, Appl
Sequence 46, Appl
Sequence 51, Appl
Sequence 1714, Ap
Sequence 8, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 6596, Ap
Sequence 1, Appl
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Sequence 49, Appl
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Sequence 5299, Ap
Sequence 45, Appl
Sequence 50, Appl
Sequence 42, Appl
Sequence 53, Appl
Sequence 54, Appl
Sequence 5297, Ap
Sequence 10692, A
Sequence 299, App
Sequence 723, App
Sequence 5345, Ap
Sequence 17509, A
Sequence 47, Appl
Sequence 13474, A
Sequence 12994, A

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US-10-027-632-12994

ALIGNMENTS

RESULT :

US-10-286-926-2
; Sequence 2, Application US/10286926
; Publication No. US20030175752A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457CON
; CURRENT APPLICATION NUMBER: US/10/286,926
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1799
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

LOCATION: (245)...(1529)
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1718)
 OTHER INFORMATION: n = adenine or guanine or cytosine or thymidine
 US-10-286-926-2

Query Match 99.8%, Score 1794.8; DB 12; Length 1799;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1799; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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1	CGCGGCTCGCGCGCAAGGCTGGCGCGCGCGCGCTTTCCCTTGTTCCCTGGTCAACAAGAA	60
61	TGTGGAGTGTCTGGCTGAATCCTCATACAGACAAGATCATTTATGGTGTGTAGGTGA	120
61	TGTGGAGTGTCTGGCTGAATCCTCATACAGACAAGATCATTTATGGTGTGTAGGTGA	120
121	AAAAGTGTATATCAAGGACCAAGGAGGAGAAATTCAGAGGAGGAGAAATTTGCTCT	180
121	AAAAGTGTATATCAAGGACCAAGGAGGAGAAATTCAGAGGAGGAGAAATTTGCTCT	180
181	GCAGGTGTGCGAGCAGGATGCTTCTGCAACAAAGGCTCCACCCAGCCACATCTTGGGA	240
181	GCAGGTGTGCGAGCAGGATGCTTCTGCAACAAAGGCTCCACCCAGCCACATCTTGGGA	240
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301	GCCTGTCTCCACAGAAACAGCAGACATGTTTGGAGGATGCTTCTCTCTTCATGT	360
301	GCCTGTCTCCACAGAAACAGCAGACATGTTTGGAGGATGCTTCTCTCTTCATGT	360
361	GCCCATCAATGTGAGGCGCCAGCCTTGTATGAAATATGTTGATGAGGAGGAGCACTG	420
361	GCCCATCAATGTGAGGCGCCAGCCTTGTATGAAATATGTTGATGAGGAGGAGCACTG	420
421	GAATCGAAATTCATGTTTACACCTTTGTGAGAAATGCCAGCAGACGTTCCAAATCTAG	480
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901	AAATCTCTAGGGGTACTCTCACTTCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATA	960
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 ; Sequence 2, Application US/10091085
 ; Publication No. US2002014672A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ford, John
 ; APPLICANT: Mulero, Julio
 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL, CD39-LIKE
 ; FILE OF INVENTION: POLYPEPTIDES
 ; FILE REFERENCE: 28110/35761
 ; CURRENT APPLICATION NUMBER: US/10/091,085
 ; CURRENT FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: 09/350,836
 ; PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: 09/273,447
 PRIOR FILING DATE: 1999-03-19
 PRIOR APPLICATION NUMBER: 09/118,205
 PRIOR FILING DATE: 1998-07-16
 PRIOR APPLICATION NUMBER: 09/122,449
 PRIOR FILING DATE: 1998-07-24
 PRIOR APPLICATION NUMBER: 09/244,444
 PRIOR FILING DATE: 1999-02-04
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2

LENGTH: 1799

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (246) ..(1529)

NAME/KEY: misc_feature

LOCATION: (1718)

OTHER INFORMATION: n = adenine or guanine or cytosine or thymine

S-10-091-085-2

Query Match 99.8%; Score 1794.8; DB 13; Length 1799;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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y	61	TG	TGGAGTGTCTTGGGTGAATCTCTACAGCAAGATCAATATGTTGTGTAGTTGA	120
b	61	TG	TGGAGTGTCTTGGGTGAATCTCTACAGCAAGATCAATATGTTGTGTAGTTGA	120
y	121	AA	AGTGTATATTAAGGACCAAGAGAAATTCAGAGGAAAGAAATTCGCTT	180
b	121	AA	AGTGTATATTAAGGACCAAGAGAAATTCAGAGGAAAGAAATTCGCTT	180
y	181	GC	AGGTGTGCGCAGAGATGCTTCTGCAAAAGGCTCCACCCAGCCACATCTTGGGA	240
b	181	GC	AGGTGTGCGCAGAGATGCTTCTGCAAAAGGCTCCACCCAGCCACATCTTGGGA	240
y	241	AA	GAATGGCAGCTTCTGGGCAAGTCTTTTATGCTGGTGTATCTGTGTGGA	300
b	241	AA	GAATGGCAGCTTCTGGGCAAGTCTTTTATGCTGGTGTATCTGTGTGGA	300
y	301	GC	CTGTCTCCACAGAACACAGAGACTTGGTTGAGGGTATCTTCTGTCTTCATGT	360
b	301	GC	CTGTCTCCACAGAACACAGAGACTTGGTTGAGGGTATCTTCTGTCTTCATGT	360
y	361	GC	CCCATCAATGTGAGCGCCAGCAGCTTGTATGGAATTAATGTTGATGAGGAGCACTG	420
b	361	GC	CCCATCAATGTGAGCGCCAGCAGCTTGTATGGAATTAATGTTGATGAGGAGCACTG	420
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b	421	GA	ACTCGAATTCATGTTTACCTTTGTGCAAAATGCCAGACAGCTTCCAAATCTAG	480
y	481	AG	GGGAAGTTTGTATCTGTGAGCCAGACTTCTGCTTTGTAGATCAACCTTAAGC	540
b	481	AG	GGGAAGTTTGTATCTGTGAGCCAGACTTCTGCTTTGTAGATCAACCTTAAGC	540
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DB	841	ACCTAGGGGGAGCCTCCACCAATCAGTTCTTCCGCCAGTTTGGAGAAACTCTGGAAAC	900
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QY	1321	CCAGGGAAGTGTGTATTAACCTTGGAAATCTTCACTCAGGAGTCTTCTGTGCTATGG	1380
DB	1321	CCAGGGAAGTGTGTATTAACCTTGGAAATCTTCACTCAGGAGTCTTCTGTGCTATGG	1380
QY	1381	ATCTCAGCTACATCACAGCCCTGTAAAGGATGGCTTTGGGCTTTCAGACAGCACTCT	1440
DB	1381	ATCTCAGCTACATCACAGCCCTGTAAAGGATGGCTTTGGGCTTTCAGACAGCACTCT	1440
QY	1441	TACAGCTCAAAAGAAAGTGAACATAGACAGGGGTGGGCTTGGGGCCACCTTTC	1500
DB	1441	TACAGCTCAAAAGAAAGTGAACATAGACAGGGGTGGGCTTGGGGCCACCTTTC	1500
QY	1501	ACCTTGTGAGTCTCTGGGATCTCCCATTTGAGGCACTTCTTCTTGGAGACCTGAT	1560
DB	1501	ACCTTGTGAGTCTCTGGGATCTCCCATTTGAGGCACTTCTTCTTGGAGACCTGAT	1560
QY	1561	TTGCCAACACCTTTTAAAGGGAGAGAGACACTTAGTTCTTGAACCTAGTCTGGGACA	1620
DB	1561	TTGCCAACACCTTTTAAAGGGAGAGAGACACTTAGTTCTTGAACCTAGTCTGGGACA	1620
QY	1621	TCTCGACTTGAAGCTTAGAGATTWRGTTAATTAACGGCCGAGCTTATCTTWTATAGT	1680
DB	1621	TCTCGACTTGAAGCTTAGAGATTWRGTTAATTAACGGCCGAGCTTATCTTWTATAGT	1680
QY	1681	AATTTACTTGTGTCGCGCTTACAGCTGTGTATGGNAAACCTGCGTCCCAACTAACGC	1740
DB	1681	AATTTACTTGTGTCGCGCTTACAGCTGTGTATGGNAAACCTGCGTCCCAACTAACGC	1740
QY	1741	TTGASAMATCCCTTTCGACAGCTGGGATACCAAGCCGACAGCGCTTCCACAGTGGCA	1799
DB	1741	TTGASAMATCCCTTTCGACAGCTGGGATACCAAGCCGACAGCGCTTCCACAGTGGCA	1799

b 1501 ACCTGTTGACAGTCTCTGGGCACTCCCAITGAGGCCACGCTACTTCTTGGAGACCTGGCA 1560
y 1561 TTGCCACACCTTTTAAAGGGAGGAGAGGCACTTGTCTGAACTAGTCTGGGGACA 1620
p 1561 TTGCCACACCTTTTAAAGGGAGGAGAGGCACTTGTCTGAACTAGTCTGGGGACA 1620
y 1621 TCCTGGACTTGAGCCTAGAGATTWRGTAAATTAASGGCGGAGCTTATCCTTWTATAGGT 1680
p 1621 TCCTGGACTTGAGCCTAGAGATTWRGTAAATTAASGGCGGAGCTTATCCTTWTATAGGT 1680
y 1681 AATTACTTCCMTGGCGGCTTTACAGCTCGTGATGNNAACTGGTCCCAACTAACGC 1740
b 1681 AATTACTTCCMTGGCGGCTTTACAGCTCGTGATGNNAACTGGTCCCAACTAACGC 1740
y 1741 TTGASAMATCCCTTTCGACCTCGGATACCAAAAGCCGACGCGCTTCCACAGTGCCA 1799
b 1741 TTGASAMATCCCTTTCGACCTCGGATACCAAAAGCCGACGCGCTTCCACAGTGCCA 1799

RESULT 4
S-10-286-926-24
Sequence 24 Application US/10286926
Publication No. US2003075752A1
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 28110/36457CON
CURRENT APPLICATION NUMBER: US/10/286,926
PRIOR FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,235
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/122449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/244444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 1601
TYPE: DNA
ORGANISM: Homo sapiens
S-10-286-926-24

Query Match 80.3% Score 1445; DB 12; Length 1601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/ 1 GCGGGCTGCGCGCAAGGGTGGCGCGCGCGTTCCTTGTTCCTGGTCAACAAGAAA 60
2 1 GCGGGCTGCGCGCAAGGGTGGCGCGCGTTCCTTGTTCCTGGTCAACAAGAAA 60
/ 61 TGTGGAGTGTCTGGCTGATCCTCATACAGCAAGATCATTTATGCTGTAGTTGA 120
3 61 TGTGGAGTGTCTGGCTGATCCTCATACAGCAAGATCATTTATGCTGTAGTTGA 120
/ 121 AAAAGTGATATAATAAGGAACCAAGGAGAAAATTCAGAGGAGAAAGAAAATTCGCTCT 180
3 121 AAAAGTGATATAATAAGGAACCAAGGAGAAAATTCAGAGGAGAAAGAAAATTCGCTCT 180

QY 181 GCAGGTGTGGAGCAGGATTGCTTCTGCAACAAAGCCTCCACCAGCAGCATCTTGGGA 240
DB 181 GCAGGTGTGGAGCAGGATTGCTTCTGCAACAAAGCCTCCACCAGCAGCATCTTGGGA 240
QY 241 AAAGAATGGCCACTTCTTGGGGCACAGCTTTTTCATGCTGGTGGTATCCTGTCTTCAATGT 300
DB 241 AAAGAATGGCCACTTCTTGGGGCACAGCTTTTTCATGCTGGTGGTATCCTGTCTTCAATGT 300
QY 301 GCGCTGTCTCCACAGAACCCAGCAGACTTGGTTTGAAGGTATCTTCTGTCTTCAATGT 360
DB 301 GCGCTGTCTCCACAGAACCCAGCAGACTTGGTTTGAAGGTATCTTCTGTCTTCAATGT 360
QY 361 GCCCATCAATGTCCAGCCAGCAGCTTGTATGCAATTAATGTTGATGCAAGGAGCAGCTG 420
DB 361 GCCCATCAATGTCCAGCCAGCAGCTTGTATGCAATTAATGTTGATGCAAGGAGCAGCTG 420
QY 421 GAATCTCGAATTCATGTTTACACCTTTGTGAGAAAATGCCAGGACAGCTTCCAAATTCAG 480
DB 421 GAATCTCGAATTCATGTTTACACCTTTGTGAGAAAATGCCAGGACAGCTTCCAAATTCAG 480
QY 481 AAGGGGAAGTTTTCATCTTGTGAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGC 540
DB 481 AAGGGGAAGTTTTCATCTTGTGAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGC 540
QY 541 AGGGTGTGTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGGAAGTC 600
DB 541 AGGGTGTGTGAGACCGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCGGAAGTC 600
QY 601 ACTGGAAGGAGACCCCAAGTGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC 660
DB 601 ACTGGAAGGAGACCCCAAGTGTCTTAAAGGCAACAGCAGGACTACGCTTACTGCCAGAAC 660
QY 661 ACAAAGCCAGGCTCTCTCTTTGAGGTAAAGAGATCTTCAGGAACTCAGCTTCTCTGG 720
DB 661 ACAAAGCCAGGCTCTCTCTTTGAGGTAAAGAGATCTTCAGGAACTCAGCTTCTCTGG 720
QY 721 TACCAAGGGCAGTGTTAGCATCATGATCCGACGAAGGCATATTAGCTTGGGTTA 780
DB 721 TACCAAGGGCAGTGTTAGCATCATGATCCGACGAAGGCATATTAGCTTGGGTTA 780
QY 781 CTGTGAATTTCTGACAGGTGAGTGTGATGCGCACAGACAGAGACTGTGGGACCTTGG 840
DB 781 CTGTGAATTTCTGACAGGTGAGTGTGATGCGCACAGACAGAGACTGTGGGACCTTGG 840
QY 841 ACCTAGGGGAGCCTCCACCAAAATCACGTTTCTTCCGCGAGTTTGAGAAAATCTTGAAC 900
DB 841 ACCTAGGGGAGCCTCCACCAAAATCACGTTTCTTCCGCGAGTTTGAGAAAATCTTGAAC 900
QY 901 AAATCTCTAGGGGCTACCTCACTTCTTTCAGATGTTTAAACAGCATTATAAGCTTATA 960
DB 901 AAATCTCTAGGGGCTACCTCACTTCTTTCAGATGTTTAAACAGCATTATAAGCTTATA 960
QY 961 CACATAGTTACCTGGGATTTGGATTGAAGCTCCAGACTAGCAACCTCGGAGCCCTGG 1020
DB 961 CACATAGTTACCTGGGATTTGGATTGAAGCTCCAGACTAGCAACCTCGGAGCCCTGG 1020
QY 1021 AGACAGAAGGAGCTGATGGGCACACTTTCGGAGTGCCTGTTTACCAGATGTTTGAAG 1080
DB 1021 AGACAGAAGGAGCTGATGGGCACACTTTCGGAGTGCCTGTTTACCAGATGTTTGAAG 1080
QY 1081 CAGAGTGGATCTTTTGGGGGTGTGAATACCAAGTATGTTGCGCAACCAAGAGGGAGGTGG 1140
DB 1081 CAGAGTGGATCTTTTGGGGGTGTGAATACCAAGTATGTTGCGCAACCAAGAGGGAGGTGG 1140
QY 1141 GCTTTGAGCCCTGTATGCCAGTGTGCTGAGGCTGTGACAGGAAACTTCCAGCCAG 1200
DB 1141 GCTTTGAGCCCTGTATGCCAGTGTGCTGAGGCTGTGACAGGAAACTTCCAGCCAG 1200
QY 1201 AGGAGGTCCAGAGAGGTTCCTTCTATGCTTCTTCTTACTATTATGACGAGCTGTGACA 1260
DB 1201 AGGAGGTCCAGAGAGGTTCCTTCTATGCTTCTTCTTACTATTATGACGAGCTGTGACA 1260

1261 CAGACATGATTGATTATGAAAGGGGGGTTATTTAAAGTTGAAGATTTTGAAGAAAG 1320
|||||
1261 CAGACATGATTGATTATGAAAGGGGGGTTATTTAAAGTTGAAGATTTTGAAGAAAG 1320
|||||
1321 CCAGGGAAGTGTGTGATAACTTGGAAAACTTCACTCAGGCAGTCTTCTCCCTGTGCATGG 1380
|||||
1321 CCAGGGAAGTGTGTGATAACTTGGAAAACTTCACTCAGGCAGTCTTCTCCCTGTGCATGG 1380
|||||
1381 ATCTCAGCTACATCAGAGCCCTGTAAAGGATGGCTTTGCGTTTGAGACAGACAGTCT 1440
|||||
1381 ATCTCAGCTACATCAGAGCCCTGTAAAGGATGGCTTTGCGTTTGAGACAGACAGTCT 1440
|||||
1441 TACAG 1445
|||||
1441 TACAG 1445
|||||

RESULT 5

S-10-092-063-24
Sequence 24, Application US/10092063
Publication No. US20020173005A1
GENERAL INFORMATION:
APPLICANT: Ford, John
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD33-LIKE POLYPEPTIDES
FILE REFERENCE: 28110/35908
CURRENT APPLICATION NUMBER: US/10/092,063
CURRENT FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-39
PRIOR APPLICATION NUMBER: 69/273,447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 05/244,444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 1601
TYPE: DNA
ORGANISM: Homo sapiens
S-10-092-063-24

Query Match 80.3%; Score 1445; DB 13; Length 1601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/ 1 GCAGGCTGCCGCAAGGGTGGCGCGCGCTTTCCCTTGTTCCTGGTCAACAAGAAA 60
/ 1 GCAGGCTGCCGCAAGGGTGGCGCGCGCTTTCCCTTGTTCCTGGTCAACAAGAAA 60
/ 61 TGTGGAGTGTCTTGGCTGAATCCTCATACAGCAAGATCATTTATGGTGTGTAGTTGA 120
/ 61 TGTGGAGTGTCTTGGCTGAATCCTCATACAGCAAGATCATTTATGGTGTGTAGTTGA 120
/ 121 AAAAGTGATATAATAAGGAACCAAGAGAAAAATTGAGAGGAAAAAAATTTGCTCT 180
/ 121 AAAAGTGATATAATAAGGAACCAAGAGAAAAATTGAGAGGAAAAAAATTTGCTCT 180
/ 181 GCAGGCTGCCGCAAGGGTGGCGCGCGCTTTCCCTTGTTCCTGGTCAACAAGAAA 240
/ 181 GCAGGCTGCCGCAAGGGTGGCGCGCGCTTTCCCTTGTTCCTGGTCAACAAGAAA 240
/ 241 AAAGAAATGGCCACTTCTTGGGGCAGACTCTTTTCAATGCTGGTGTATCCTGTGTTGA 300
/ 241 AAAGAAATGGCCACTTCTTGGGGCAGACTCTTTTCAATGCTGGTGTATCCTGTGTTGA 300

QY 301 GCCTGTCTCCACAGGAACACAGACTTGGTTGAGGGTATCTTCTCTCTTCCATGT 360
DB 301 GCCTGTCTCCACAGGAACACAGACTTGGTTGAGGGTATCTTCTCTCTTCCATGT 360
QY 361 GCCCATCAATGTCCAGGCCAGACCTTGTATGGAATATGTTGTATGAGGAGACTG 420
DB 361 GCCCATCAATGTCCAGGCCAGACCTTGTATGGAATATGTTGTATGAGGAGACTG 420
QY 421 GAACTCGAATTCATGTTTACACCTTTGTGAGAAAAATGCCAGACAGCTTCCAAATCTAG 480
DB 421 GAACTCGAATTCATGTTTACACCTTTGTGAGAAAAATGCCAGACAGCTTCCAAATCTAG 480
QY 481 AAGGGGAAGTTTGTGATTCGTGAAGCCAGGACTTCTGCTTTTGTAGAACAACCTAAGC 540
DB 481 AAGGGGAAGTTTGTGATTCGTGAAGCCAGGACTTCTGCTTTTGTAGAACAACCTAAGC 540
QY 541 AGGGTGTGAGACCGTTCAAGGGCTCTTACAGGTGGCCAAAGACTCAATCCCGAGTC 600
DB 541 AGGGTGTGAGACCGTTCAAGGGCTCTTACAGGTGGCCAAAGACTCAATCCCGAGTC 600
QY 601 ACTGAAAAAGACCCAGTGTCTTAAAGCAACAGCAGGACTACGCTTACTGCCAGAAC 660
DB 601 ACTGAAAAAGACCCAGTGTCTTAAAGCAACAGCAGGACTACGCTTACTGCCAGAAC 660
QY 661 ACAAGCCAAAGGCTCTGCTCTTTGAGGTAAGGAGATCTTTCAGGAAAGTCACTTTCTGG 720
DB 661 ACAAGCCAAAGGCTCTGCTCTTTGAGGTAAGGAGATCTTTCAGGAAAGTCACTTTCTGG 720
QY 721 TACCAAGGGCAGTGTGATCATGATGATCCTCCAGCAAGGCAATATTAGCTTGGGTTA 780
DB 721 TACCAAGGGCAGTGTGATCATGATGATCCTCCAGCAAGGCAATATTAGCTTGGGTTA 780
QY 781 CTGTGAATTTTCTGACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 781 CTGTGAATTTTCTGACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 841 ACCTAGGGGGAGCTCCACCCAAATCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 841 ACCTAGGGGGAGCTCCACCCAAATCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 AAATCTCTAGGGGCTACCTCACTTCTTTCAGATGTTTAAACAGCACTTATAAGCTCTATA 960
DB 901 AAATCTCTAGGGGCTACCTCACTTCTTTCAGATGTTTAAACAGCACTTATAAGCTCTATA 960
QY 961 CACATAGTTTACCTGGGATTTGGATTTGAAAGTCTGCAAGCTAGCAACCTGGAGGCTG 1020
DB 961 CACATAGTTTACCTGGGATTTGGATTTGAAAGTCTGCAAGCTAGCAACCTGGAGGCTG 1020
QY 1021 AGCAGAGAGGACTGATGGGCACACTTTCCGGAGTGCCTGTTTACCGAGATGTTGGAG 1080
DB 1021 AGCAGAGAGGACTGATGGGCACACTTTCCGGAGTGCCTGTTTACCGAGATGTTGGAG 1080
QY 1081 CAGAGTGGATCTTTGGGGGTGTGAAATACCAGTATGCTGGCAACCAAGAGAGGGAGTGG 1140
DB 1081 CAGAGTGGATCTTTGGGGGTGTGAAATACCAGTATGCTGGCAACCAAGAGAGGGAGTGG 1140
QY 1141 GCTTTGAGCCCTGCTATGCCGGAAGTGTGAGGGGTGTGAGGGGTGTGAGGGGTGTGAGGG 1200
DB 1141 GCTTTGAGCCCTGCTATGCCGGAAGTGTGAGGGGTGTGAGGGGTGTGAGGGGTGTGAGGG 1200
QY 1201 AGGAGGTCCAGAGAGGTTTCTTCTATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1260
DB 1201 AGGAGGTCCAGAGAGGTTTCTTCTATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1260
QY 1261 CAGACATGATTGATTGAAAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAAG 1320
DB 1261 CAGACATGATTGATTGAAAAAGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAAAG 1320
QY 1321 CCAGGGAAGTGTGTGATAACTTGAAGAACTTCACTCAGGCAGTCTTCTCCCTGTGCATGG 1380
DB 1321 CCAGGGAAGTGTGTGATAACTTGAAGAACTTCACTCAGGCAGTCTTCTCCCTGTGCATGG 1380

1381 ATCTCAGCTACATACAGCCCTGTTAAAGATGGCTTTGGCTTTGCAGACAGCAGAGTCT 1440
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1381 ATCTCAGCTACATACAGCCCTGTTAAAGATGGCTTTGGCTTTGCAGACAGCAGAGTCT 1440
|||||
1441 TACAG 1445
|||||
1441 TACAG 1445

RESULT 6

S-10-286-926-4
Sequence 4, Application JS/10286926
Publication No. US20030175752A1
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Young, George
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 28110/36457CON
CURRENT APPLICATION NUMBER: US/10/286,926
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: 09/357,900
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 09/350836
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273447
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 09/122449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/244444
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1287
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1284)
S-10-286-926-4
Query Match 71.5%; Score 1287; DB 12; Length 1287;
Best Local Similarity :00.0%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
246 ATGGCCACTTCTTGGGGCAGTCTTTTCATGCTGGTGATTCCTGTTTGCAGCGCT 305
1 ATGGCCACTTCTTGGGGCAGTCTTTTCATGCTGGTGATTCCTGTTTGCAGCGCT 60
306 GTCTCCACAGAACCCAGAGACTTGGTTGAGGGTATCTCTGTCCTCCATGTCGCC 365
61 GTCTCCACAGAACCCAGAGACTTGGTTGAGGGTATCTCTGTCCTCCATGTCGCC 120
366 ATCAATGTTCAGCCCGCAGCCTTTGTATGGAATTTATGTTGATCGAGGAGCAGTCTGA 425
121 ATCAATGTTCAGCCCGCAGCCTTTGTATGGAATTTATGTTGATCGAGGAGCAGTCTGA 180
426 CGAATTCATGTTTACACCTTTGTCAGAAAATGCCAGACAGCTTCCAATTCAGAAAGG 485
181 CGAATTCATGTTTACACCTTTGTCAGAAAATGCCAGACAGCTTCCAATTCAGAAAGG 240
486 GAAGTTTTCATCTCTGAGCCAGAGACTTCTGCTTTTGTAGATCAACTAAGCAGGT 545
|||||

RESULT 7

US-10-091-085-4

241 GAAGTTTTTGATTTCTGTSAAGCCAGGACTTTTGTCTTTTGTAGATCAACCTTAAGCAGG 302
QY
546 GCTCAGACCGTTCAAGGGCTTTAGAGCGTGGCCAAAGACTCAATCCCGCAAGTCACTGG 605
DB
301 GCTGAGACCGTTCAAGGGCTTTAGAGCGTGGCCAAAGACTCAATCCCGCAAGTCACTGG 360
QY
606 AAAAGAGACCCAGTGGTCTTAAGAGGCAACAGCAGGACTACGCTTACTGCCAGAACACAAA 665
DB
361 AAAAGAGACCCAGTGGTCTTAAGAGGCAACAGCAGGACTACGCTTACTGCCAGAACACAAA 420
QY
666 GCCAAGGCTCTGCTCTTTGAGGTAAGAGGACTCTTACGGAAGTCACTTTCTCTGGTACCA 725
DB
421 GCCAAGGCTCTGCTCTTTGAGGTAAGAGGACTCTTACGGAAGTCACTTTCTCTGGTACCA 480
QY
726 AAGGCGAGTGTAGCATCATGGATGCGAGGAGGCATATTAGCTTGGGTTACTGTG 785
DB
481 AAGGCGAGTGTAGCATCATGGATGCGAGGAGGCATATTAGCTTGGGTTACTGTG 540
QY
786 AATTTTCTGACAGCTCAGCTGCTATGGCCACAGACAGGAGACTGTGGGGACCTTTGGACCTA 845
DB
541 AATTTTCTGACAGCTCAGCTGCTATGGCCACAGACAGGAGACTGTGGGGACCTTTGGACCTA 600
QY
846 GGGGAGGCTCCACCCAAATCACGTTCTGCGCCAGTTTGAGAAAACCTCTGGAACAACT 905
DB
601 GGGGAGGCTCCACCCAAATCACGTTCTGCGCCAGTTTGAGAAAACCTCTGGAACAACT 660
QY
906 CCTAGGGGCTACCTCACTTCTTTGAGATGTTTAAACAGACTTATAGCTCTATACACAT 965
DB
661 CCTAGGGGCTACCTCACTTCTTTGAGATGTTTAAACAGACTTATAGCTCTATACACAT 720
QY
966 AGTTTACCTGGGATTTGGAATGAAAGCTGCAAGCTAGCAACCTCTGGAGGACCTCTGGAGACA 1025
DB
721 AGTTTACCTGGGATTTGGAATGAAAGCTGCAAGCTAGCAACCTCTGGAGGACCTCTGGAGACA 780
QY
1026 GAAGGAGCTGATGGGCACACTTTCCGAGGTGCTGTTTACCGAGATGTTTGGAGAGCAG 1085
DB
781 GAAGGAGCTGATGGGCACACTTTCCGAGGTGCTGTTTACCGAGATGTTTGGAGAGCAG 840
QY
1086 TGGATCTTTGGGGGTGTGAAATACAGTATGTTGGCAACCAAGAGGAGGAGTGGGCTTT 1145
DB
841 TGGATCTTTGGGGGTGTGAAATACAGTATGTTGGCAACCAAGAGGAGGAGTGGGCTTT 900
QY
1146 GAGCCTCTGATGCCGAAGTCTGAGGGTGTACGAGGAAACCTTCCACAGCCAGAGGAG 1205
DB
901 GAGCCTCTGATGCCGAAGTCTGAGGGTGTACGAGGAAACCTTCCACAGCCAGAGGAG 960
QY
1206 GTCCAGAGAGGTTCCCTTCTATGCTTTCTTACTTATTTACCCAGAGCTGTTCACACAGAC 1265
DB
961 GTCCAGAGAGGTTCCCTTCTATGCTTTCTTACTTATTTAGCCAGAGCTGTTCACACAGAC 1020
QY
1266 ATGATTGATTATGAAAAGGGGGGTATTTTAAAGTTTGAAGATTTTGAAGAAAAGCCAGG 1325
DB
1021 ATGATTGATTATGAAAAGGGGGGTATTTTAAAGTTTGAAGATTTTGAAGAAAAGCCAGG 1080
QY
1326 GAAGTGTGTATTAACCTTGGAAAACCTTCCCTCAGGAGTCTTTCTCTGTCGATGGATCTC 1385
DB
1081 GAAGTGTGTATTAACCTTGGAAAACCTTCCCTCAGGAGTCTTTCTCTGTCGATGGATCTC 1140
QY
1386 AGCTACATCACAGCCCTGTTTAAAGGATGGCTTTTGGCTTTTGCAGACAGCAGTCTTACAG 1445
DB
1141 AGCTACATCACAGCCCTGTTTAAAGGATGGCTTTTGGCTTTTGCAGACAGCAGTCTTACAG 1200
QY
1446 CTCACAAAGAAAGTGAACACATAGACAGGCTGGGCTTTGGGGGCCACCTTTACCTG 1505
DB
1201 CTCACAAAGAAAGTGAACACATAGACAGGCTGGGCTTTGGGGGCCACCTTTACCTG 1360
QY
1506 TTGCAGTCTCTGGGCACTCTCCCATTTGA 1532
DB
1261 TTGCAGTCTCTGGGCACTCTCCCATTTGA 1287

Sequence 4, Application US/10091085

Publication No. US2002c146772A1

GENERAL INFORMATION:

APPLICANT: Ford, John

APPLICANT: Mulero, Julio

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE

TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 28110/35761

CURRENT APPLICATION NUMBER: US/10/091,085

CURRENT FILING DATE: 2002-03-05

PRIOR APPLICATION NUMBER: 09/350,836

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: 09/273,447

PRIOR FILING DATE: 1999-03-19

PRIOR APPLICATION NUMBER: 09/118,205

PRIOR FILING DATE: 1998-07-16

PRIOR APPLICATION NUMBER: 09/122,449

PRIOR FILING DATE: 1998-07-24

PRIOR APPLICATION NUMBER: 09/244,444

PRIOR FILING DATE: 1999-02-04

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 4

LENGTH: 1287

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(1284)

S-10-091-065-4

Query Match 71.5%; Score 1287; DB 13; Length 1287;
Best Local Similarity 100.0%; Pred. NC. C;
Matches 1287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 246 ATGCCACTCTTGGGGACAGCTTTTTCATGCTGGTGTATCTCTGTGTTCACGGCT 305
D 1 ATGCCACTCTTGGGGACAGCTTTTTCATGCTGGTGTATCTCTGTGTTCACGGCT 60
Y 306 GTCTCCACAGAACACAGCAGACTTGGTTTGGAGGTATCTCTGTCTCCATGTCCGCC 365
D 61 GTCTCCACAGAACACAGCAGACTTGGTTTGGAGGTATCTCTGTCTCCATGTCCGCC 120
Y 366 ATCAATGTCAGCCAGCAGCCTTGTATGGAATATGTTGATGACGGAGCAGCTGGAAT 425
D 121 ATCAATGTCAGCCAGCAGCCTTGTATGGAATATGTTGATGACGGAGCAGCTGGAAT 180
Y 426 CGAATTCATGTTTACACCTTTGTCAGAAAATGCCAGACAGCTTCCAATTCAGAGGG 485
D 181 CGAATTCATGTTTACACCTTTGTCAGAAAATGCCAGACAGCTTCCAATTCAGAGGG 240
Y 486 GAAGTTTGTATCTGTGAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGCAGGT 545
D 241 GAAGTTTGTATCTGTGAAGCCAGGACTTCTGCTTTTGTAGATCAACCTAAGCAGGT 303
Y 546 GCTGAGACCGTTCAGGGCTCTTAGAGGTGSCCAAGACTCAATCCCGAAGTCACTG 605
D 301 GCTGAGACCGTTCAGGGCTCTTAGAGGTGSCCAAGACTCAATCCCGAAGTCACTG 360
Y 606 AAAAGACCCAGTGGTCTTAAGGCCAACAGCAGACTAGCTTACTGCCAGACACAA 665
D 361 AAAAGACCCAGTGGTCTTAAGGCCAACAGCAGACTAGCTTACTGCCAGACACAA 420
Y 666 GCCAAGGCTGCTCTTGTAGGTAAAGGAGATCTCAGGAAGTCACTTCTGTTACCA 725
D 421 GCCAAGGCTGCTCTTGTAGGTAAAGGAGATCTCAGGAAGTCACTTCTGTTACCA 480
Y 726 AAGGCAGTGTAGCATCATGATGATGATGATGATGATGATGATGATGATGATGATG 785
D 481 AAGGCAGTGTAGCATCATGATGATGATGATGATGATGATGATGATGATGATGATG 540
Y 786 AATTTCTGACAGGTGAGTGGTGGCCACAGACAGAGACTGTGGGAGCTTGGACCT 845
D 845 AATTTCTGACAGGTGAGTGGTGGCCACAGACAGAGACTGTGGGAGCTTGGACCT

RESULT 8

US-10-092-063-4

; Sequence 4, Application US/10092063

; Publication No. US20020171005A1

; GENERAL INFORMATION:

; APPLICANT: Ford, John

; APPLICANT: Mulero, Julio

; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES

; FILE REFERENCE: 28110/35908

; CURRENT APPLICATION NUMBER: US/10/092,063

; CURRENT FILING DATE: 2002-03-05

; PRIOR APPLICATION NUMBER: 09/370,265

; PRIOR FILING DATE: 2002-01-31

; PRIOR APPLICATION NUMBER: PCT/US99/16:80

; PRIOR FILING DATE: 1999-07-16

; PRIOR APPLICATION NUMBER: 09/350,836

; PRIOR FILING DATE: 1999-07-09

; PRIOR APPLICATION NUMBER: 09/273,447

; PRIOR FILING DATE: 1999-03-19

; PRIOR APPLICATION NUMBER: 09/244,444

; PRIOR FILING DATE: 1999-02-04

; PRIOR APPLICATION NUMBER: 09/122,449

PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1287
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1284)
S-10-092-063-4

Query Match		71.54;	Score 1287;	DB 13;	Length 1287;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 1287;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
y	246	ATGCCCACTCTCTGGGACAGTCTTTTTCATGCTGGTGTATCTCTCTGCTTCCATGTGCCCC	305		
b	1	ATGCCCACTCTCTGGGACAGTCTTTTTCATGCTGGTGTATCTCTCTGCTTCCATGTGCCCC	60		
y	306	GTCTCCACAGAACACAGCAGACTTGTGTTGAGGGTATCTTCTCTGCTTCCATGTGCCCC	365		
b	61	GTCTCCACAGAACACAGCAGACTTGTGTTGAGGGTATCTTCTCTGCTTCCATGTGCCCC	120		
y	366	ATCAATGTCAGCGCCAGCACCTTGTATGGAATATGTTTGTATGAGGAGCACTTGAACCT	425		
b	121	ATCAATGTCAGCGCCAGCACCTTGTATGGAATATGTTTGTATGAGGAGCACTTGAACCT	180		
y	426	CGAATTCATGTTTACACCTTTGTGCAGAAAATGCCAGGACAGCTTCCAAATCTAGAAAGG	485		
b	181	CGAATTCATGTTTACACCTTTGTGCAGAAAATGCCAGGACAGCTTCCAAATCTAGAAAGG	240		
y	486	GAAGTTTGTGATCTGTGAGCCAGGACTTCTGCTTTGTAGATCAACTAGACAGGT	545		
y	241	GAAGTTTGTGATCTGTGAGCCAGGACTTCTGCTTTGTAGATCAACTAGACAGGT	300		
y	546	GCTGAGCCGTTCAAGGGCTCTTAGAGGTGCCAAAGACTCAATCCCGGAAGTCACTGG	605		
y	301	GCTGAGCCGTTCAAGGGCTCTTAGAGGTGCCAAAGACTCAATCCCGGAAGTCACTGG	360		
y	606	AAAAAGCCCCAGTGTCTTAAGGGAACAGAGGACTAGCTTATGCCAGNACAA	565		
y	361	AAAAAGCCCCAGTGTCTTAAGGGAACAGAGGACTAGCTTATGCCAGNACAA	420		
y	666	GCCAAAGGCTCTGCTCTTTGAGGTAAAGAGATCTTCCAGGAAGTCACTTCTGTTACCA	725		
y	421	GCCAAAGGCTCTGCTCTTTGAGGTAAAGAGATCTTCCAGGAAGTCACTTCTGTTACCA	480		
y	726	AAGGGAGTGTAGCATCATGATGGATGGATCCGACGAAGGCATATAGCTGGGTTACTGTG	785		
y	481	AAGGGAGTGTAGCATCATGATGGATGGATCCGACGAAGGCATATAGCTGGGTTACTGTG	540		
y	786	AATTTCTGCAGGTCACTGCTGATGGCCACAGACAGAGACTGTGGGACCTTGGACCTA	845		
y	541	AATTTCTGCAGGTCACTGCTGATGGCCACAGACAGAGACTGTGGGACCTTGGACCTA	600		
y	846	GGGGAGCCCTCCACCCAAATCAAGTTCCTCCCGAGTTTGAGAAAACCTTGGAACAACT	905		
y	601	GGGGAGCCCTCCACCCAAATCAAGTTCCTCCCGAGTTTGAGAAAACCTTGGAACAACT	660		
y	906	CCTAGGGCTACCTCACTCTTGTAGATGTTTAAAGAGACTTAAAGCTCTATACAT	965		
y	661	CCTAGGGCTACCTCACTCTTGTAGATGTTTAAAGAGACTTAAAGCTCTATACAT	720		
y	966	AGTTACCTGGGATTTGAAAGTGAAGAGCTAGCAACCTCGGAGCCCTGGAGACA	1025		
y	721	AGTTACCTGGGATTTGAAAGTGAAGAGCTAGCAACCTCGGAGCCCTGGAGACA	780		
y	1026	GAAGGGACTGATGGGACACTTTCCGAGTGCCTGTTTACCGAGATGGTTGGAAGCAGAG	1085		
y	781	GAAGGGACTGATGGGACACTTTCCGAGTGCCTGTTTACCGAGATGGTTGGAAGCAGAG	840		

QY	1086	TGATCTTTGGGGTGTGAATACAGATATGGTGGCAACCAAGAAAGGGAGGTGGSCCTTT	1145
DB	841	TGATCTTTGGGGTGTGAATACAGATATGGTGGCAACCAAGAAAGGGAGGTGGSCCTTT	900
QY	1146	GAGCCCTGCTATGCCGAAGTCTGAGGGTGTACGAGGAAACCTTACCAGCCAGAGGAG	1205
DB	901	GAGCCCTGCTATGCCGAAGTCTGAGGGTGTACGAGGAAACCTTACCAGCCAGAGGAG	960
QY	1206	GTCCAGAGAGGTTCTTCTATGCTTTCTCTTACTATATGACCGAGCTGTTACACAGAC	1265
DB	961	GTCCAGAGAGGTTCTTCTATGCTTTCTCTTACTATATGACCGAGCTGTTACACAGAC	1020
QY	1266	ATGATTCATTATGAAAGAGGGGTATTTTAAAGTTTGAAGATTTTGAAGAAAGCCAGG	1325
DB	1021	ATGATTCATTATGAAAGAGGGGTATTTTAAAGTTTGAAGATTTTGAAGAAAGCCAGG	1080
QY	1326	GAAGTGTGTGATTAACCTTGGAAAACCTTCACTCAGGAGTCTTCTCTGTGCAATGATCTC	1385
DB	1081	GAAGTGTGTGATTAACCTTGGAAAACCTTCACTCAGGAGTCTTCTCTGTGCAATGATCTC	1140
QY	1386	AGCTACATCACGCCCTGTAAAGGATGCTTTGGCTTTGCAGACAGACAGTCTTACAG	1445
DB	1141	AGCTACATCACGCCCTGTAAAGGATGCTTTGGCTTTGCAGACAGACAGTCTTACAG	1200
QY	1446	CTCAAAAGAAAGTGAACACATAGAGACGGGCTGGGCTTTGGGGGCCACCTTTTACCTG	1505
DB	1201	CTCAAAAGAAAGTGAACACATAGAGACGGGCTGGGCTTTGGGGGCCACCTTTTACCTG	1260
QY	1506	TTGCAGTCTCTGGGCATCTCCCATTTGA	1532
DB	1261	TTGCAGTCTCTGGGCATCTCCCATTTGA	1287

RESULT 9
US-10-286-326-6
; Sequence 6, Application US/10286926
; Publication No. US20030175752A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457CON
; CURRENT APPLICATION NUMBER: US/10/286,326
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

LOCATION: (1) .. (1284)

S-10-286-926-6

Query Match

Best Local Similarity 99.5%; Pred. No. 0;

Matches 1281; Conservative 0; Mismatch 0

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1	ATGGCCACTTCTTGGGCGACAGTCTTTTTCATGCTGTGGTATCTCTGTGTTTGAGCGCT	60
306	GTCTCCACAGAAACAGACACTTGGTTTGAGGATCTCTTCTGTCTTCCATCTGCCCG	365
61	GTCCTCCACAGAACACGACACTTGGTTTGAGGATCTCTTCTGTCTTCCATCTGCCCG	120
366	ATCAATGTACGGCGCAGCACCTTGTATGGAAATTATGTTTGTATGAGGAGCACTTGGAACT	425
121	ATCAATGTACGGCGCAGCACCTTGTATGGAAATTATGTTTGTATGAGGAGCACTTGGAACT	180
426	CGAATTCATGTTTACACCTTGTGCAGAAATGCGAGGACAGCTTCCAATCTTAGAGGG	485
181	CGAATTCATGTTTACACCTTGTGCAGAAATGCGAGGACAGCTTCCAATCTTAGAGGG	240
486	GAAGTTTTGATCTGTGAAACAGGACTTCTCTCTTTGTAGATCAACCTTAAGCAGGCT	545
241	GAAGTTTTGATCTGTGAAACAGGACTTCTCTCTTTGTAGATCAACCTTAAGCAGGCT	300
546	GCTCAGACCGTTCAAGGCTCTTAGAGGTGCGCAAGACTCAATCTCCCGGAGTCACTGG	605
301	GCTGAGACCGTTCAAGGCTCTTAGAGGTGCGCAAGACTCAATCTCCCGGAGTCACTGG	360
606	AAAAGACCCCAAGTGGTCTTAAAGCAACACGAGACTTACGCTTACTGCCAGAACACAAA	665
361	AAAAGACCCCAAGTGGTCTTAAAGCAACACGAGACTTACGCTTACTGCCAGAACACAAA	420
666	GCCAAAGCTCTGCTCTTTGAGGTAAGAGAGATCTTTCAGGAAGTCACTTTCCTGGTACCA	725
421	GCCAAAGCTCTGCTCTTTGAGGTAAGAGAGATCTTTCAGGAAGTCACTTTCCTGGTACCA	480
726	AAGGCAGTGTTAGCATCATGGATCGGATCCGACGAAGGCAATTAGCTTGGGTTACTGTG	785
481	AAGGCAGTGTTAGCATCATGGATCGGACGAAGGCAATTTCGCTTGGGTTACTGTG	540
786	AATTTTTCGACAGTCACTGCGCCACACAGAGAGACTGTGGGACCTTGGACCTA	845
541	AATTTTTCGACAGTCACTGCGCCACACAGAGAGACTGTGGGACCTTGGACCTA	600
846	GGGGAGGCTCCACCCAAATCACGTTCTGCCCCAGTTTGAGAAACTCTCGGAACAACT	905
601	GGGGAGGCTCCACCCAAATCACGTTCTGCCCCAGTTTGAGAAACTCTCGGAACAACT	660
906	CCTAGGGCTACCTCACTTCCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACACAT	965
661	CCTAGGGCTACCTCACTTCCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACACAT	720
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721	AGTTACCTGGGATTTGGATTCGAAGCTCCAGACTAGCAACCTTGGGAGCCCTGGAGCA	780
1026	GAAGGACTGATGGGCACACTTTCGGAGTGCCTGTTTACCGAGATGTTTGGAAAGCAGAG	1085
781	GAAGGACTGATGGGCACACTTTCGGAGTGCCTGTTTACCGAGATGTTTGGAAAGCAGAG	840
1086	TGGATCTTTGGGGTGTGAATACCACTATGGTGGCAACCAAGAGAGGGAGCTGGGCTTT	1145
841	TGGATCTTTGGGGTGTGAATACCACTATGGTGGCAACCAAGAGAGGGAGCTGGGCTTT	900
1146	GAGCCCTGCTATGCCCAAGTGTCTGAGGGTGTAGAGGAAACTCTACCAGCCAGAGAGAG	1205
901	GAGCCCTGCTATGCCCAAGTGTCTGAGGGTGTAGAGGAAACTCTACCAGCCAGAGAGAG	960
1206	GTCCAGAGAGTTCCTTCTATGCTTCTTACTATTATGACCGAGCTGTTGACACAGAC	1265

151 CGAATTCATGTTTACACCTTTGTGCAGAAATGCGAGACAGCTTCCAATTCAGAGGG 240

486 GAAGTTTTTGATCTGTGAAGCCAGGACTTTCTGCTTTTGAGATCAACCTTAAGCAGGGT 545

241 GAAGTTTTTGATCTGTGAAGCCAGGACTTTCTGCTTTTGAGATCAACCTTAAGCAGGGT 300

546 GCTGAGACCGTTCAAGGGCTCTTAGAGTGGCCAAAGACTCAATCCCGCAAGTCACTGG 605

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361 AAAAAGACCCCAAGTGGTCTTAAAGCAACAGCAGACTACGCTTTACTGCCAGAACACAAA 420

666 GCCAAGGCTCTGCTCTTTGAGSTAAGGAGATCTTCAGGAAGTCACTTTCTCTGGTACCA 725

421 SCCAAGGCTCTGCTCTTTGAGSTAAGGAGATCTTCAGGAAGTCACTTTCTCTGGTACCA 480

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481 AAGGCGAGTGTAGCATCATGGATGGATCCGACGAAGGCATATTAGCTTGGTTTACHTGTG 540

786 AATTTCTGACAGTCACTTCGATGGGCCACAGACAGGAGACTGTGGGACCTTGGACCTA 845

541 AATTTCTGACAGTCACTTCGATGGGCCACAGACAGGAGACTGTGGGACCTTGGACCTA 600

846 GGGGAGCGCTCACCCAAATCACGTTCTGCCCCAGTTTGAGAAACTCTCGGACAAACT 905

601 GGGGAGCGCTCACCCAAATCACGTTCTGCCCCAGTTTGAGAAACTCTCGGACAAACT 660

906 CTTAGGGCTACCTCACTTCCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACACAT 965

661 CTTAGGGCTACCTCACTTCCTTTGAGATGTTTAAACAGCACTTATAAGCTCTATACACAT 720

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721 AGTTACCTGGGATTTGGATTCAGAGCTGCAGACTAGCAACCTTGGAGCCCTGGAGACA 780

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1086 TGGATCTTTGGGGTGTGAATACAGATATGGTGGCAACCAAGAGGGGAGGTGGGCTTT 1145

941 TGGATCTTTGGGGTGTGAATACAGATATGGTGGCAACCAAGAGGGGAGGTGGGCTTT 900

1146 GAGCCCTGCTATGCGCGAAGTGTGAGGGTGTGACAGGAAACTTCACCAAGCCAGAGGAG 1205

901 GAGCCCTGCTATGCGCGAAGTGTGAGGGTGTGACAGGAAACTTCACCAAGCCAGAGGAG 960

1206 GTCCAGAGGTTCTCTCTAATGCTTTCTTACTATTATGACCGAGTGTGTACACAGAC 1265

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1021 ATGATTGATTATGAAGAGGGGGTATTTTAAAGTGAAGATTTTGAAGAAAGCCAGG 1080

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1141 AGCTACATCACAGCCCTGTTTAAAGATGGCTTTGGCTTTTGAGACAGACAGACTTTACAG 1200

1446 CTCACAAAGAAAGTGAAACAATACAGACGGGCTGGGCTTTGGGGGCCACTTTACCTG 1505

1201 CTCACAAAGAAAGTGAAACAATACAGACGGGCTGGGCTTTGGGGGCCACTTTACCTG 1260

1506 TTGCAGTCTCTGGGCATCTCCCAITGA 1532

Db 126i TTGCAGTCTCTGGGCATCTCCCATTTGA 1287

RESULT 11

US-13-092-063-6

; Sequence 6, Application US/10092063

; Publication No. US20020173005A1

; GENERAL INFORMATION:

; APPLICANT: Ford, John

; APPLICANT: Mulero, Julio

; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES

; FILE REFERENCE: 28110/35908

; CURRENT APPLICATION NUMBER: US/10/092,063

; CURRENT FILING DATE: 2002-03-05

; PRIOR APPLICATION NUMBER: 09/370,265

; PRIOR FILING DATE: 2002-01-31

; PRIOR APPLICATION NUMBER: PCT/US99/16180

; PRIOR FILING DATE: 1999-07-16

; PRIOR APPLICATION NUMBER: 09/350,836

; PRIOR FILING DATE: 1999-07-09

; PRIOR APPLICATION NUMBER: 09/273,447

; PRIOR FILING DATE: 1999-03-19

; PRIOR APPLICATION NUMBER: 09/244,444

; PRIOR FILING DATE: 1999-02-04

; PRIOR APPLICATION NUMBER: 09/122,449

; PRIOR FILING DATE: 1998-07-24

; PRIOR APPLICATION NUMBER: 09/118,205

; PRIOR FILING DATE: 1998-07-16

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 1287

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; .NAME/KEY: CDS

; .LOCATION: (1)..(1284) .

US-10-092-063-6

421 CCCAAGGCTCTGCTCTTTGAGGTAAAGAGATCTTCAGGAAGTCAACCTTCTCTGGTACCA 480
 726 AAGGCGAGTGTAGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 785
 481 AAGGCGAGTGTAGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
 786 AATTCTTGACAGGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 845
 541 AATTCTTGACAGGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
 846 GGGGAGGCTCCACCCAAATCACCTTCTGCCCCAGTTTGAGAAACTCTGGAACT 905
 601 GGGGAGGCTCCACCCAAATCACCTTCTGCCCCAGTTTGAGAAACTCTGGAACT 660
 906 CCTAGGGCTACCTCAGTCTCTTGTAGATGTTTAAAGAGCTTTATAGCTCTTATACAT 965
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 1026 GAAGGAGCTGATGGGACACTTTCCGAGTGCCTGTTTACCGAGATGTTTGAAGCAGAG 1085
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 1021 ATGATTCATATGAAAGGGGGTATTTAAAGTTCAGATTTGAAAGAAAGCCAGG 1080
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 1201 CTCACAAAGAAAGTGAACATAGACAGCGGCTGGGCTTTGGGSCCACCCTTTCACCTG 1260
 1506 TTGCAGTCTCTGGSCATCTCCCATTTGA 1532
 1261 TTGCAGTCTCTGGSCATCTCCCATTTGA 1287

RESULT 12

S-09-925-299-103

Sequence 103, Application US/09925299

Patent No. US2002055627A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA102

CURRENT APPLICATION NUMBER: US/09925,299

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US06/05883

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1556
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 103
 LENGTH: 1457
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-925-299-103

Query Match 60.5% Score 1089.2; DB 9; Length 1457;
 Best Local Similarity 99.0%; Pred. No. 0;
 Matches 1085; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

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 QY 613 CCCAGTGGTCTCTAAAGCAACAGCAGGACTTACGCTTACTGCCAGAACACAAAGCCAAAG 672
 DB 74 CCCAGTGGTCTCTAAAGCAACAGCAGGACTTACGCTTACTGCCAGAACACAAAGCCAAAG 133
 QY 673 CTCCTCTTTGAGTAAAGAGATCTTACAGAAATCACTTTCTCGTACCAAGGCA 732
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 QY 733 GTGTTAGCATCATGATCGATCCGACGAGGACATATAGTTGGTTACTCTGGAATTTTC 792
 DB 194 GTGTTAGCATCATGATCGATCCGACGAGGACATATAGTTGGTTACTCTGGAATTTTC 253
 QY 793 TGACAGGTGAGTCTGATCGCCACACAGACAGAGAGTCTGTGGGACCTTGGACCTAGGGGAG 852
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 DB 554 TTGGGGGTGTGAAATACCAATGATGTTGSCAACCAAGAGGGAGTGGGCTTTCAGGCCCT 613
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 DB 854 TCACAGCCCTCTTAAAGATGGCTTTGGCTTTGCAGACAGCAGCTCTTACAGCTACAA 913
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JS-10-198-846-12729

Query Match 26.5%; Score 476; DB 14; Length 978;
Best Local Similarity 86.1%; Pred. No. 1.1e-142;
Matches 632; Conservative 0; Mismatches 87; Indels 15; Gaps 9;

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|||
255: CACCAGGACATCTGTGAAAGATGGACATCTCTGGGSCACAGCTCTTTTCATGCT 314
|||
281: GGTGTATTCCTGTGTTCAGCGGTGTCTCCACAGGAAACCAGAGACTTTGGTTGAGG 340
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315: GGTGTATTCCTGTGTTCAGCGGTGTCTCCACAGGAAACCAGAGACTTTGGTTGAGG 374
|||
341: TATCTTCCTGTCTCCATGTGCCCATCAATGTGAGGCGCAGGACCTTGATGGAAATAT 403
|||
375: TATCTTCCTGTCTCCATGTGCCCATCAATGTGAGGCGCAGGACCTTGATGGAAATAT 434
|||
401: GTTTCATGAGGAGGACTTGGAAATCGAATCATGTGTACACCTTTGTGCAGAAATGCC 463
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435: GTTTCATGAGGAGGACTTGGAAATCGAATCATGTGTACACCTTTGTGCAGAAATGCC 494
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461: AGGACAGCTTCATCTTAGAAGGGAAGTCTTTGATCTGTGAGGCGAGACTTTCTGC 520
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495: AGGACAGCTTCATCTTAGAAGGGAAGTCTTTGATCTGTGAGGCGAGACTTTCTGC 553
|||
521: TTTTCATGATCAACCTTAAGCAGGCTGTGAGAGCGTTCAGAGCGTCTTAGAGGTGGCAA 580
|||
554: TTTTCATGATCAACCTTAAGCAGGCTGTGAGAGCGTTCAGAGCGTCTTAGAGGTGGCAA 612
|||
581: AGACTCAATCCCCCGAAGTCACTGGAAAGAACCCAGTGTCTTAAAGGCAACAGCAGG 640
|||
612: AGACTCAATCCCCCGAAGTCACTGGAAAGAACCCAGTGTCTTAAAGGCAACAGCAGG 669
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641: ACTAGCTTACTGCCAGAACCAAGCCAGGCTCTGTCTTTGAGGTAAAGAGATCTT 700
|||
670: CTACGCTTTACTGNCAGAAACAAAGCCAGGCTCTTCTGTTGAGGTAAGGAGATCTT 727
|||
701: CA-GGAAGTCACTTCTCTGTGACCAAGGCGAGTGTAGCATCATGATGGATCCGAG 759
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RESULT 15

JS-09-960-352-11752

Sequence 11752, Application US/09960352

Patent No. US20020137139A1

GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.

APPLICANT: Tao, Nengbing

APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

FILE OF INVENTION: KJSC:5 AND FAT DEPOSITION

FILE REFERENCE: 16511.006/37-21(102991C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 11752

LENGTH: 420

TYPE: DNA

ORGANISM: Bos taurus

OTHER INFORMATION: Clone ID: 50-LIB34-029-Q1-E1-E6

JS-09-960-352-11752

Query Match 20.0%; Score 359.2; DB 10; Length 420;

Best Local Similarity 91.0%; Pred. No. 4e-105;

Matches 382; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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DB 181 TCACCTTTCTCGTACCAAGTGTAGCATCATGGATGGATCCGATGAGGCACTA 240
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DB 241 TTAGCTTGGGTTTACTGTGAATTTTCTGACAGGTCAAGTGTGATGGCCACAGCAGGAGACT 300
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DB 301 GTGGGACCTTGGACCTAGGGGGAGCCTCCACCCAAATCATGTTCTTCCCTCCAGTTTGGAG 360
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|||
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Search completed: October 6, 2003, 14:34:37

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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title: US-10-092-063-2

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maximum DB seq length: 2030000000

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database :

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6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pn:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_man:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rnd:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Length	DB ID	Description
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2	1084	60.3	4014 11	AK081435 Mus muscu
3	1083.8	60.2	4091 11	AK036641 Mus muscu
4	1082.2	60.2	2517 11	AK031581 Mus muscu

5	1081.4	60.1	2124 11	AK088455
6	1085.6	59.2	1861 11	AK079267
7	1064.4	59.2	1861 11	AK037736
9	1063.2	59.1	2070 11	AK002618
9	1059.2	58.9	4884 11	AK045828
10	882.4	49.0	1107 12	BM24818
11	761.4	42.3	842 12	B1258902
12	692.6	38.5	749 12	B1765978
13	681	37.9	801 12	B1551795
14	649	36.1	878 10	BG702864
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25	467.8	26.0	527 10	BF073260
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ALIGNMENTS

RESULT 1
AK080265

LOCUS
DEFINITION

AK080265 3698 bp mRNA linear HTC 05-DEC-2002
Mus musculus 3 days neonate thymus cDNA, R-KEN full-length enriched library, clone:A63007L13 product:ectonucleoside triphosphate diphosphohydrolase 5, full insert sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

AK080265 3698 bp mRNA linear HTC 05-DEC-2002
Mus musculus 3 days neonate thymus cDNA, R-KEN full-length enriched library, clone:A63007L13 product:ectonucleoside triphosphate diphosphohydrolase 5, full insert sequence.

AK080265

AK080365.1 GI:26348444

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.

1

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

10349636

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159


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553 553 CGTTCAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCGCGAAGTACTCTCGAAAAAGA 612
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613 613 CCCAGTGTCTTAAAGCAACAGCAGGAGTACTGCTTACTGCGCAGAACACAAAGCCAGG 672
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673 673 CTCTGCTCTTTCAGGTAAAGGAGACTCTTCAGGAAGTCACTTTCTCTGTCACCAAGGCA 732
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DEFINITION Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
library, clone:Cl30017F05, product:ectonucleoside triphosphate
diphosphohydrolase 5, full insert sequence.
ACCESSION AK081435
VERSION AK081435.1 Gi:26349158
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Katsunari, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishire, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Chara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 984 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
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Carninci, P., de Bernaldo, M.F., Brownstein, M.C., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
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Marchionni, L., Mashima, J., Mazzarelli, C., Mommaerts, P., Nordone, P.,
Rig, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seva, T., Shibata, Y., Storch, K.F., Suzuki, H.,
Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S.
and Hayashizaki, Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 12011014
PUBMED 12011014
REFERENCE 6
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
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Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imoant, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurirara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akai, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE
Direct Submission

JOURNAL
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

FEATURES

Location/Qualifiers

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BASE COUNT

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Query Match

60.3%; Score 1084; DB 11; Length 4014;

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Matches 1292; Conservative 0; Mismatches 270; Indels 16; Gaps 3;

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Y 728 GGGCAGTGTGTAGCATCATGATGATCCGACAGAGGATATTAGCTTGGGTTACTGTGAA 787
D 714 TGGCAGGCTTAGCATCATGATGATGGTCTTATGAAGGCATACACTAGTCTTACCCTGAA 773
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Y 1268 GATTTGATTAAGAGGGGGGTATTTTAAAGTTGAAGATTTTGAAGAAAGAAAGCCAGGGA 1327

[illegible]

IPRGYLTSEFMENSIKFLYTHSYLGLKXARLALGALEAKGTGDTGHTSRACLRWJ
ERWIFGGVXIQIGGQEGMEFPCYAEVRVQKHQPEVRSQSAFYAFSYIFDR
AAATH::DYKGGVGLXVEDFERKAREVCDNLGFSFGSPFLCMLDYITALLKDPGF
ADGTLQLTKVNNIETGVALGATFHLQSLGITS*
ASE COUNT 998 a 943 c 992 g 1158 t
RIGIN

Query Match 60.2%; Score 1093.8; DB 11; Length 4091;
Best Local Similarity 82.0%; Pred. No. 2.9e-223;
Matches 1290; Conservative 0; Mismatches 267; Indels 16; Gaps 3;

22 GCGGCGCGGCTTTCCCTTGCTCCCTGCTCAACAGAAATGTCGAGTGTCTTGCCCTGAAAT 81
18 GCGGCGCGGCGCGGCGCTTTGCTTGACACAGAAATGAAGAGTGTATGCTGAAAT 77
82 CCTCATACAGAAAGATCAATATGTCGCTCTAGTTTGAAAGAAAGTATATAAAGGAA 141
78 CTTCAAGCAGAGGCGATCATATGACCTCTCTTTTAAATGGCTGGGTGACCCGCCA 137
142 CCNAGGAGAAATTT-----CAGNAGAAAGAAATTTGCCCTCGAGGTGTCGA 132
138 CTTGGTGTAAAGAGAACCGGCCAAAGGAGGCGCTGAAAGSACCTCCACAGAGGTGTGA 137
193 GCAGGATTTGCTTCTGCAACAAAGCCTCCACCCAGCCACATCTTGGAAAGAAATGGCCA 252
198 GCAGCACTGCTTCAGAACAAA-----GCCTCAGCTCCACATCTTGGAAAGAAATGGCCA 253
253 CTTCTGGGGCAGAGTCTTTTCAATGCTGTGGTATGCTCTGTTTSCAGGCTGTCTCC 312
254 CTTCTGGGGGCTGTGTC---TTCAATGCTGTATAGCTCTGTTTGGCAGCACTGTCTCT 310
313 ACAGAAACCCAGCAGCTGTTTGGAGGATCTTCTGCTCTCCATGTCGCCCATCAATG 372
311 ACAGAGAACGACAGCTGTTTGAAGGTGCTTCTTGTCTTCCATGTGCCCTTTAAATG 370
373 TCAGCGCCAGCAGCTTGTATGGAATATGTTTATGATGAGGAGGACATGGAACCTCGAATTC 432
371 TCAGTCCCGCACCTTTATGGAATATGTTTATGATGCGGCACAGCTGGAACCTCGGATTC 430
433 ATGTTTACACTTTTGCAGAAATGCGAGACAGCTTCCAAATCTAGAAAGGGAATTT 492
431 ATGTTTACACTTTTGCAGAAATGCGAGACAGCTTCCCTCTTCTGGAAGGTGAAATTT 490
493 TTGATTTCTGTAAGCCAGGACTTTCTCTTTTGTAGATCAACCTTAGCAGGCTGTGAGA 552
491 TTGATTTCTGTAAGCCAGGACTTTCTCTTTTGTGATCAGCCCAACAGGCTGTGAGA 550
553 CCGTTCAGGCGCTTTAGAGTGGCCAAAGACTCAATCCCCCGAAGTCACTGGAAGAAAGA 612
551 CTGTCCAGGAGCTTTGAGGTGGCCAAAGACTCGATCCCGCAGAGCCACTGGGAAAGGA 610
613 CCCAGTGGTCCCTAAGGCAACAGCAGACTACGCTTACTGCGCAGACACAAAGCCAGG 672
611 CCCCGTGGTCTGAAAGCAACGCGCGGACTCGCTTGTGCTGCTGAGCAGAAAGCCAGG 670
673 CTCTGCTCTTTGAGTAAAGGAGATCTTCAGGAGTCACTTCTGTTTCCGTACCAAGAGGCA 732
671 CTCTGCTCTTTGAGGTAGAGGAGATCTTCAAGATTTCACTTTCTGTTCCAGATGGCA 730
733 GTGTTAGATCATGATGGATGCGACGAGGATATTTAGCTTGGTTCATGTTGAAATTTTC 792
731 GCGTTAGATCATGATGGATGGGTCTTATGAAGCATPACTAGCTTGGTTACCGTGAATTTTC 790
793 TGACAGGTCACTGCTCATGGCCACAGCAGGAGACTGTGGGACCTTGGACCTAGGGGGAG 852
791 TAAAGGTCACTGCTCATGGTCTGTGCGCAGGAGACTGTGGGACCTTGGACCTGGGGGTG 850
853 CCTCCAGCCAAATCACGTTCTCTGCCCGCAGTTTGAGAAATCTTGGAAACAAATCTCCAGGG 912
851 CCTCCAGCCAAATCACGTTCTTACCCAGTTTGAGAAATCTTGGAAACAAATCTCCAGGG 910
913 GCTACCTCACTCTCTTTGAGATGTTTAAAGCAGCTTATAAGCTCTTATACATAGTTACC 972

911 GCTACCTCACTCTCTTTGAGATGTTTAAACAGCAGCTTTAACTCTCTACACATAGTTACT 970
973 TGGGATTTGGATTTGAAAGCTGCAAGACTAGCAACCTCGGGAGCCCTGGAGACAGAAGGGA 1032
971 TGGGATTTGGACTGAAAGCTGCAAGACTGCAACTCTCTGGAGGCCCTGGAGCAAAAGGGA 1030
1033 CTGATGGGCACACTTTCGGAGTGGCTGTCTTACAGAGATGGTTGGAAGCAGAGTGGATCT 1032
1031 CTGATGGGCACACTTTCGAAAGTGGCTGTCTTACCAAGATGGTTGGAAGCAGAGTGGATCT 1030
1093 TTGGGGGTGTGAAATACCAATACCAATGATGTTGCAAGAGGAGGAGTGGGCTTTGAGGCCCT 1152
1091 TTGGGGGTGTGAAATACCAATACCAATGATGTTGCAAGAGGAGGAGTGGGCTTTGAGGCCCT 1150
1153 GCTATGCGCAAGTGTGAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1212
1151 GCTATGCGCAAGTGTGAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1210
1213 GAGGTTCCTCTTATGCTTTCTCTTACTTATGACGAGCTGTTGACACAGACATGATG 1272
1211 GAAGGCCCTTCTACGCTTTCTCTTACTTATGACGAGCTGAGGAGGAGGAGGAGGAGGAGGAG 1270
1273 ATTATGAAAGAGGGGGGTATTTTAAAGTTGAAGATTTTGAAGAGAAAGCCAGGAGGAGTGT 1332
1271 ATTATGAAAGAGGGGGGTATTTTAAAGTTGAAGATTTTGAAGAGAAAGCCAGGAGGAGTGT 1330
1333 GTGATACTTGGGAAACTTCACTCAGGAGTCTTCTCTGCTGTGATGATCTCAGCTTACA 1392
1331 GTGACAACTTGGGAGAGCTTCTCTCGGAGAGTCTCTCTCTGATGAGCTTCACTTACA 1390
1393 TCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGACAGCAGCAGCAGCTTTACAGCTTCAAA 1452
1391 TCACAGCCCTGTTAAAGGATGGCTTTGGCTTTGACAGCAGCAGCAGCTTTACAGCTTCAAA 1450
1453 AGAAGTGAACCAACATAGAGAGGCTGGGCTTTGGGCGCCACCTTTCACTTTCAGCTTTCAGCT 1512
1451 AGAAGTGAACCAACATAGAGAGTGGTGGGCTTTGGGCGCCACCTTTCACTTTCAGCTTTCAGCT 1510
1513 CTCTGGGATCTCCCATGAGGCGCAGCTACTTCTCTGAGAGCTGCTTTTCCAGACCTT 1572
1511 CTCTGGGATCTCCCATGAGGCGCAGCTTCCACCTCTTGAAGCTGCTTCTTGAAGCTT 1570
1573 TTTTAAAGGGGAGG 1585
1571 TTTTCAAGGAGG 1583

RESULT 4
AK031581
LOCUS
DEFINITION
AK031581 2517 bp mRNA linear HTC 05-DEC-2002
Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
enriched library, clone:6030456F04 product:ectonucleoside
triphosphate diphosphohydrolase 5, full insert sequence.

ACCESSION AK031581
VERSION AK031581.1 GI:26327434
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PubMed 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374

PUBMED REFERENCE AUTHORS	11042159	3	Shibata, K., Itoh, M., Aizawa, K., Nagacka, S., Sasaki, M., Carrinci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hachima, M., Nishimura, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuno, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
PUBMED REFERENCE AUTHORS	11076861	4	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamakawa, I., Saito, T., Okazaki, Y., Gotohori, T., Bono, H., Kasukawa, T., Saito, R., Kadoya, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, T., Pesole, G., Quackenbush, J., Schiraldi, L., Stauber, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carrinci, P., de Bonaldo, M., Brownstein, M. J., Butt, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, J., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Teyo-oka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, J., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
PUBMED REFERENCE AUTHORS	1:217851	5	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
PUBMED REFERENCE AUTHORS	6 (bases 1 to 2517)	6	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carrinci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, I., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, Y., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Xuramatsu, M. and Hayashizaki, Y.
PUBMED REFERENCE AUTHORS	Submitted (16-JUL-2001)	7	Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp). URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
PUBMED REFERENCE AUTHORS	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	8	Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/
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PUBMED REFERENCE AUTHORS	URL: http://genome.gsc.riken.go.jp/	80	URL: http://genome.gsc.

494	TTGATTCTGTGAAGCCGGGACTTTCTGCTTTTGTGGATCAGCCCAAAACAGGGTCTCAGA	553	RESULT 5	AK088455	2124 bp	mRNA	linear	HTC 05-DEC-2002	
553	CCGTTCAAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGGAAAAAGA	612	LOCUS	AK088455				Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN	
554	CTGTCCAGGAGCTCTTGGAGGTGGCCAAAGACTCGATCCCCCAGAAGCACTGGGAAAGGA	613	DEFINITION					full-length enriched library, clone:E43018A.6	
613	CCCCAGTGGTCTTAAGGCAACAGCAGGACTACGCTTACTCTGCAGCAACACAAAGCCAAAG	672						product:ectonucleoside triphosphate diphosphohydrolase 5, full	
614	CCCCGGTGGTCTGAAGACCAACGGCCGAGTCCGTTTGCCTGCCTGAGCAGAAAGCCCAAG	673						insert sequence.	
673	CTCTGCTCTTTGAGGTAAAGGAGATCTTCAGGAGTCACTTCTCGTACCAAGGSCA	732	ACCESSION	AK088455	1	GI:26353463			
674	CTCTGCTCTTTGAGGTAGAGAGATCTTCAGGAGTCACTTCTCGTCCGATGSCA	733	VERSION	AK088455.1				HTC; CAP trapper.	
733	GTGTTAGCATCATGGATGGATCCGACGAGGCAATATTAGCTTTGGGTTACTGTGAATTTTC	792	KEYWORDS					Mus musculus (house mouse)	
734	CGGTTAGCATCATGGATGGGCTTATGAAGGCACTAGCCCTGGTTACCGTGAACCTTC	793	SOURCE					Mus musculus	
793	TGACAGGTCAGCTGATCGCCACAGCAGGAGACTGTGGGACCTTGGACCTAGGGGGAG	852	ORGANISM						
794	TAAACAGTCAGCTGATCGTGTGGCCAGGAGACTGTGGGACCTTGAACCTGGGGGGTG	853	REFERENCE						
853	CTCCACCCAAATCACTGCTCTGCCCCAGTTTGAGAAACCTCTGGAACAACTCTAGGG	912	AUTHORS	Carninci, P. and Hayashizaki, Y.					
854	CTCCACCCAAATCACTGCTCTACCCAGTTTGAGAAACCTCTGGAACAACTCTAGGG	913	TITLE	High-efficiency full-length cDNA cloning					
913	GCTAGCTCACTTCTTGAATGTTTAAACAGCACTTATAGCTCTTAAACAGCATAGTTACC	972	JOURNAL	Meth. Enzymol. 303, 19-44 (1999)					
914	GCTAGCTCACTTCTTGAATGTTTAAACAGCACTTATAGCTCTTAAACAGCATAGTTACT	973	MEDLINE	99279253					
973	TGGGATTTGGATTGAAGCTGCAAGCTAGCAACCTGGGAGCCCTGGAGACAGGGA	1032	PUBMED	10349636					
974	TGGGATTTGGACTGAAGCTCAAGACTGGCACTCTGGAGCCCTGGAGCAAGGGA	1033	REFERENCE						
1033	CTGATGGGCACACTTTCGGAGTGCTGTTTACCGAGATGTTTGAAGCAGAGTGGATCT	1092	AUTHORS	Carninci, P., Shibata, Y., Hayatsu, K., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, Y. and Hayashizaki, Y.					
1034	CTGATGGACATACGTTTGAAGTGCTGTTTACCAAGATGTTTGAAGCAGAGTGGATCT	1093	TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes					
1093	TTGGGGGTGTGAATACCACTATGTTGGCAACCAAGAGGGGAGTGGCTTTGAGCCCT	1152	JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)					
1094	TTGGGGGTGTGAATACCACTATGTTGGCAACCAAGAGGGGAGTGGCTTTGAGCCCT	1153	MEDLINE	20499374					
1153	GCTATGCCGAAGTGTGAGGTGGTACGAGAAACCTTCCAGCCAGGAGGATCCAGA	1212	PUBMED	11076861					
1154	GCTATGCCGAAGTGTGAGGTGGTACGAGAAACCTTCCAGCCAGGAGGATCCAG	1213	REFERENCE						
1213	GAGTTCCTCTTATGCTTCTTACTATTATGACCGAGCTGTTGACACAGCATGATTCG	1272	AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishii, K., Kiyosawa, H., Kondo, S., Yamakawa, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Buit, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Nombarts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.					
1274	GAAGCGCCTTCTACGTTTCTTACTAGTCTAGCTGAGCCGCTGACACACACTTGATCG	1273	TITLE	Functional annotation of a full-length mouse cDNA collection					
1273	ATTATGAAGAGGGGGTATTTAAAGTTGAAGATTTTGAAGAAAGCCAGGGAAGTGT	1332	JOURNAL	Nature 409 (6821), 685-690 (2001)					
1274	ATTATGAAGAGGGGGTATTTAAAGTTGAAGATTTTGAAGAAAGCCAGGGAAGTGT	1333	MEDLINE	21085660					
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1393	TCACAGCCCTGTTAAGAGTGGCTTGGCTTTCGAGACAGCAGCATCTTACAGCTACAA	1452	AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.					
1394	TCACAGCCCTGTTGAAGATGTTTGGCTTTCGCGAGCGCACCTCTTACAGCTACAA	1453	TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs					
1453	AGAAAGTGAACAACTAGACAGCGGCTGGGCTTGGGGGCCACCTTTTCCACTGTTCAGT	1512	JOURNAL	Nature 420, 563-573 (2002)					
1454	AGAAAGTGAACAACTAGACAGCTGTTGGGCTTGGGGGCCACCTTTTCCACTGTTCAGT	1513	MEDLINE						
1513	CTCTGGGATCTCCATTTAGGCGCAGTCTTCTCTTGGAGACCTTGCATTTGCCAACCT	1572	PUBMED						
1514	CTCTGGGATCTCCATTTAGGCGCAGTCTTCCACTCTCGAAGCTTGCATTTCTGAACGTT	1573	REFERENCE						
1573	TTTTAAGGGAGG	1585	AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.					
1574	TTCTCACAGGAG	1586	TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs					
			JOURNAL	Nature 420, 563-573 (2002)					

db 1134 TGCGGAGTCTGAGGCTAGTACAGGGGAAACTTCACCAGCCAGCAAGTCCAGGAAG 1193

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db 1254 TGAAGAGGGGGGTTTAAAGTTGAAGATTTTGAAGAAAGCCAGGGAAGTGTGTGA 1313

2y 1337 TAACCTGGAAGAACTTCACCTCAGGAGCTCTTCTCTGTCATGGATCTGACATCATCAC 1396

2b 1314 CAACCTGGGAGCTTCTCTCGGAGCTCTTCTCTGTCATGGATCTGACATCATCAC 1373

2y 1397 AGCCTGTTAAGGATGCTTGGCTTGGAGACAGACAGCTTACAGCTCACAAGAA 1456

db 1374 AGCCTGTTAAGGATGCTTGGCTTGGAGACAGACAGCTTACAGCTCACAAGAA 1433

2y 1457 AGTGAACAACATAGAGCGGCTCGGCTTGGGCGCCACCTTTCACCTGTTGGAGTCTCT 1516

db 1434 AGTGAACAACATAGAGCTGTTGGGCTTGGGCGCCACCTTTCACCTGTTGGAGTCTCT 1493

2y 1517 GGGATCTCCCATTTGAGCCGACCTACTCTCTGGAGACCTGTCATTTCCCAACACCTTTT 1576

2b 1494 GGGATCACCAGCTGAGGCCAAGCTCCACCTCTGAGCTTGCACTTCTGAGAGCTTTCT 1553

2y 1577 AAGGGGAGG 1585

db 1554 CACAGGAAG 1562

RESULT 6

AK079267

LOCUS

DEFINITION Mus musculus adult male urinary bladder cDNA, Riken full-length enriched library, clone:9530068A17 product:ectonucleoside triphosphate diphosphohydrolase 5, full insert sequence.

ACCESSION AK079267

VERSION 1

KEYWORDS HTC, CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Chara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,

Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yananaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, I., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)

21085660

11217851

5

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 1661)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, Y., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyas, S., Kurthara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akhiba, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/

URL: http://fantom.gsc.riken.go.jp/

location/Qualifiers

1. .1661

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

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/db_xref="taxon:10090"

/clone="9530068A17"

/sex="male"

/tissue type="urinary bladder"

/clone lib="RIKEN full-length enriched mouse cDNA library"

/dev stage="adult"

94. .1377

/note="unnamed protein product; ectonucleoside triphosphate diphosphohydrolase 5 (MGD|MG1:1321385, GS|NM_007647, evidence: BLASTN, 99%, match=2:06)

CDS

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TPRGLTSPFMSNTKLYTHSLHGLKGAARLALIGLEAKGTGHTFRSKAPRL
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ASE COUNT 403 a 390 c 450 g 418 t
RIGIN

Query Match 59.2%; Score 1065.6; DB 11; Length 1661;
Best Local Similarity 85.2%; Pred. No. 2.2e-219;
Matches 1215; Conservative 0; Mismatches 204; Indels 7; Gaps 2:

y 160 AGGAAGAAAATAATGCTCTGTCAGGTGTCCGAGCAGATTGCTTCTGCAACAAAGCCT 219
b 12 AGGAGGAGAGCTGCTCCACAGGAGTGTGAGCAGCTGCTTCAGCAACAA-----G 67

y 220 CCACCCAGCCACATCTTTGGGAAAGAAATGCCACTTCTTGGGGCAAGTCTTTTTCATGC 279
c 68 CCTCAGGTCCACATCTTTGGGAAGAATAATGCCACTTCTTGGGGGGCTGC---TTCATGC 124

y 280 TGGTGGTATCCTGTGTTGTCAGCGCTGCTCCACAGGACAGCAGACTTGGTTGAGG 339
c 125 TGATCATAGCTGGCTTGGCAGACTGCTTCTACAGAACAGCAGACTGGTTGAAG 184

y 340 GTATCTTCTGCTTCTGATGTCCTCCCAATATGTGTCAGCGCCAGCCTTGTATGGAATTA 399
c 185 GTGCTCTTCTGCTTCTGATGTCCTCCCAATATGTGTCAGCGCCAGCCTTGTATGGAATTA 244

y 400 TGTGTGATGAGGAGACTGGAAGTCTGATTCGATGTTTACACTTGTGTCAGAAATGC 459
c 245 TGTGTGATGCGGGGAGCACTGGAAGTCTGATTCGATGTTTACACTTGTGTCAGAAATGC 304

y 460 CAGGACAGCTCCCAATCTTGAAGGGGAAGTGTGATCTGTGAAGCCAGACCTTCTG 519
c 305 CAGGACAGCTCCCTTCTTGAAGGGGAAGTGTGATCTGTGAAGCCAGACCTTCTG 364

y 520 CTTTGTAGATCAACCTTAAGCAGGGTCTGAGACGTTTCAAGGCTCTTAGAGTGCGCA 579
c 365 CTTTGTGATCAGCCCAACAAACAGGGTCTGAGACTGTCCAGGAGCTTGTGAGGTGGCCA 424

y 580 AAGACTCAATCCCGGAGTCACTGGAAAAGAGCCCGAGTGTCTTAAAGGCAACAGCAG 639
c 425 AAGACTCGATCCCGAGAGCCACTGGAAAAGAGCCCGGTTGTTTGAAGACACAGCGCC 484

y 640 GACTACGCTTACTGCCAGAACACAAAGCCAGCTCTGCTCTTTGAGGTAAAGAGATCT 699
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y 700 TCAGGAGTCACTTCTGCTGATCCAAAGGCGAGTGTACATCATGATGATGATCCGAGC 759
c 545 TCAAGATTCACCTTCTGCTGATCCAAAGGCGAGTGTACATCATGATGATGATGATG 604

y 760 AAGGCAATTAAGCTTGGGTACTGTGAATTTTCTGACAGCTGAGCTGCATGGCCACAGAC 913
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y 820 AGGAGACTGTGGGACCTTGAACCTAGGGGAGGAGCTCCACCCAAATACGTTCTGCCCC 879
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y 880 AGTTTGAGAAACTCTGGAACAAACTCTAGGGGCTACCTCACTTCTTGGAGATCTTA 939
c 725 AGTTTGAGAAACTCTGGAACAAACTCTAGGGGCTACCTCACTTCTTGGAGATCTTA 784

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1300 TTGAAGATTTTGAAGAAAGCCAGGAAAGTGTGATTAACCTTGGAAACTTCACTCAG 1359
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1360 GCAGTCTTCTGTCATGATGATCTCAGCTACATCACAGCCCTGTTTAAAGGATGCTTGT 1419
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RESULT 7
AK037736 1861 bp mRNA linear HTC 05-DEC-2002
LOCUS Mus musculus 16 days neonate thymus cDNA, RIKEN full-length
DEFINITION enriched library, clone:A130044A06 product:ectonucleoside
triphosphate diphosphohydrolase 5, full insert sequence.
ACCESSION AK037736
VERSION AK037736.1 GI:26332261
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PubMed 10349636
REFERENCE
AUTHORS Carninci,P., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PubMed 11042159
REFERENCE
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Katsurai,T., Tashiro,H., Itoh,M.,

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Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishire, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohata, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)

20530913
11076861

4

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Kawai, J., Shiragawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Harada, A., Fukunishi, Y., Konno, H., Adachi, S., Fukuda, S., Aizawa, K., Izawa, M., Nishikawa, K., Miyosawa, H., Kondo, S., Yamahara, I., Saito, T., Okazaki, Y., Goshima, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Asbunier, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pecole, G., Tomita, M., Quackenbush, J., Schrim, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okado, P., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.C., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kaniya, M., Lee, N.H., Lyons, P., Marchionni, J., Mashima, J., Mazzarelli, J., Mombarts, P., Nordone, P., Ring, B., Ringwald, V., Rodriguez, I., Sakamoto, N., Sakaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weiss, C., Whittaker, C., Wilming, L., Wyshak-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kotsuki, S., and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection Nature 409 (5621), 685-690 (2001);
21085660
11217851

5

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)

6 (bases 1 to 1861)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

Direct Submission

TITLE
JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

Location/Qualifiers
i: 186;
/organism="Mus musculus"
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FEATURES
SOURCE

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OY 294 GTTTCAGCGCTGTCTCCACAGAAACACAGACAGCTTGTGTTGAGGGTATCTTCTCTGCT 353
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further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'-GAGAGAGAGCGGCGCAACTCGATGTTTCTTTTATN 3'], cDNA was prepared by using thermostable thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGAGAGATCCAGAGTCATTAATTAATTAACCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.

FEATURES

source

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Y 276 ATGCTGGTGTATCTCTGTGTGTGGAGCGCTGTCTCCACAGGAACACGACAGCTTGTT 335
D 197 ATGCTGATCATAGCGCTGCTGGCAGCACTGTCTTCTACAGAAACACGACAGCTGGTT 256
Y 336 GAGGGTATCTCTCTCTTCCATGTGCCCATCAATGTGACGCGCCACACCTTGTATGA 395
D 257 GAAGGTGCTTCTTGTCTTCCATGTGCCCATCAATGTGACGCGCCACACCTTGTATGA 316
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Mus musculus
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1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
MEDLINE
20499374
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3
Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kutsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Hazada, A.,
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Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
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PUBMED
4
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
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Toyo-oka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S.
and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
MEDLINE
11217851
PUBMED
5
The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase 1 & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

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6 (bases 1 to 4884)

ADACHI, J., AIZAWA, K., AKIMURA, T., ARAKAWA, T., BONC, H., CARNINCI, P.,
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TAKEDA, Y., TANAKA, T., TOMARU, A., TOYA, T., YASUNISHI, A.,
MURAMATSU, M. and HAYASHIZAKI, Y.

Direct Submissions

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp).
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
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Location/Qualifiers

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AUTHORS
NIH-MGC http://mgi.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC);
JOURNAL
Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
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023. Note: this is a NIH-MGC Library."

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----- mRNA sequence.
BI258902
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
-----
1 (bases 1 to 842)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC):
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11266 row: m column: 08
High quality sequence stop: 833.
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Note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: Not I;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
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Matches 831; Conservative 0; Mismatches 7; Indels 5; Gaps 6;
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DB 61 GAGTGGCCAAAGACTCAATCCCGGAAGTCACTGGAAAAGACCCAGTGTCTCTTAAG 120
QY 630 GCAACAGCAGGACTACGCTTACTGCCAGAACACAAAGCCAAAGGCTTGTCTTTGAGTA 689
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DB 191 AAGGAGATCTTCAGGAAGTCACTTTCTGTGTACAAAGGAGCAGTGTAGCATCATGAT 240
QY 750 GGATCCGACGAGGCATATTAGCTTGGTTACTGTGTAATTTCTGACAGGTCACTGCAT 809
DB 241 GGATCCGACGAGGCATATTAGCTTGGTTACTGTGTAATTTCTGACAGGTCACTGCAT 300
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QY 870 TTCCTGCCCGGAGTTTGAGAAACTCTGGAAACAACTCTAGGGGCTACCTCACTTCCTTT 929
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 541 CGGAGTGCCTGTTTACCGAGATG-TGGAGCAGATGGAATCTTGGGGTGGAATAC 599
 1110 CAGTATGTTGCAACCAAGAGGGGA-GTGGGCTTTGAGCCCTGCTATCCGAAGTGCT 1168
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 1169 GAGGTGTTACGAGAAACTTACACCGCAGAGGAGGTCCA-GAGAGGTTTCTTCTATG 1227
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 1346 AAAC 1349
 839 AAAC 842

EST 12
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 603047264F: NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5187687 5',
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 EST B1765978.1 GI:15757556
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MSC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
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 High quality sequence stop: 749.
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 pCMV-SPORT6; Site: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 3 colons, age 26 yo male, 49 yo
 female, 71 yo male colon; 46 yo male kidney, and pool of 2
 stomachs, 62 yo male and 70 yo female. Library is
 oligo-dT primed and directionally cloned (EcoRV site is

destroyed upon cloning). Average insert size 1.4 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 023. Note: this is a NIH MGC Library."

BASE COUNT 190 a 187 c 196 g 176 t
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 Query Match 38.5%; Score 692.6; DB 12; Length 749;
 Best Local Similarity 98.6%; Pred. No. 6.2e-139;
 Matches 709; Conservative 0; Mismatches 9; Indels 1; Gaps 2;
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 QY 221 CACCCAGCCACATCTTGGGAAAGAAATGGCCACATCTTGGGGCAGCAGCTTTTTCATGCT 280
 DB 9: CACCCAGCCACATCTTGGGAAAGAAATGGCCACATCTTGGGGCAGCAGCTTTTTCATGCT 150
 QY 281 GGTGTATCTGTGTGTGACAGCGCTGTCTCCACAGGAACCCAGCAGAGCTTGTGTGAGGG 340
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 QY 761 AGGCATATTAGCTTTGGG-TTACTGTGAATTTTGTGACAGGTCACTGCTCATGCCACAGAC 819
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 QY 820 AGGACACTGTGGGACCTTGGACCTAGGGGAGGCTCCACCCCAATCACGTTCTCTGCC 878
 DB 691 AGGACACTGTGGGACCTTGGACCTAGGGGAGGCTCCACCCCAATCACGTTCTCTGCC 749

RESULT 13
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 LOCUS B1551795
 DEFINITION 603197495F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5277119 5',
 mRNA sequence.
 ACCESSION B1551795
 VERSION B1551795.1 GI:15439107
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 801)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue procurement: Miklos Paikovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1699 row: m column: 24
High quality sequence stop: 777.

FEATURES
source

1..801
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/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcagag
); Oligo-dT primed using primer 5'-TTTTTATTTTATTTN-3',
size-selected for average insert size 2.5 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NHGRI/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT
RIGIN

212 a 177 c 201 g 201 t
Query Match 37.9%; Score 681; DB 12; Length 801;
Best Local Similarity 95.0%; Pred. No. 2e-136;
Matches 757; Conservative 0; Mismatches 10; Indels 30; Gaps 4;
Y 17 GGGTGGCGCGCGGTTTCTCTGTCCTCGGTCAACAGAAATGTGGAGTCTCTGGC 76
b 5 GGGTGGCGCGCGCGGTTTCTCTGTCCTCGGTCAACAGAAATGTGGAGTCTCTGGC 64
Y 77 TGAATCCTCATACAGACAGATCATTTATGTTGCTGTT----- 113
b 65 TGAATCCTCATACAGACAGATCATTTATGTTGCTGTTAGGTAGGACTTGTATCCAGATGT 124
Y 114 -AGGTTGAAAAGTATATATAAGGAACCAAGAGAGAAATTCAGAGGAGAAAGAAA 172
b 125 AAGGTTGAAAAGTATATATAAGGAACCAAGAGAGAAATTCAGAGGAGAAAGAAA 184
Y 173 TTGCTCTGACGTTGGGAGCAGATTGCTTCTGCAACAAAGCCCTCCAGCCAGCACA 232
b 185 TTGCTCTGACGTTGGGAGCAGATTGCTTCTGCAACAAAGCCCTCCAGCCAGCACT 244
Y 233 TCTTGGGAAAAGATGGCAGCTTTCTGGGACAGACTCTTTTCATGCTGTTGGTATCTCTG 252
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Y 353 TTTCCATGTCCTCCATCATGTGAGCGCCAGCAGCCTTGTATGGAAATTATGTTTGTAGCAGG 412
b 365 TTCCATGTCCTCCATCATGTGAGCGCCAGCAGCCTTGTATGGAAATTATGTTTGTAGCAGG 424
Y 413 GAGCACTGGAATCGAATCATGTTTACCTTTGTGAGAGAAATGCGAGAGAGCTTCC 472
b 425 GAGCACTGGAATCGAATCATGTTTACCTTTGTGAGAGAAATGCGAGAGAGCTTCC 484

QY 473 AATTCTAGAGGGGAAGTTTGTGATCTGTGAAGCCAGGAGCTTCTGCTTTGTAGATCA 532
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485 AATTCTAGAGGGGAAGTTTGTGATCTGTGAAGCCAGGAGCTTCTGCTTTGTAGATCA 544
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RESULT 14

BG702864
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BG702864 878 bp mRNA linear EST 07-MAY-2001
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mRNA sequence.
BG702864
BG702864.1 GI:13974632
Homo sapiens (human)
Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue procurement: Miklos Paikovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10717 row: c column: 22
High quality sequence stop: 767.

FEATURES

source

Location/Qualifiers

1..878

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/mol_type="mRNA"

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/clone="IMAGE:4817229"

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/lab_host="DH10B"

/clone_lib="NIH_MGC_95"

/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcagag
); Oligo-dT primed using primer 5'-TTTTTATTTTATTTN-3',
size-selected for average insert size 2.5 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NHGRI/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT

ORIGIN

237 a 190 c 240 g 211 t

Query Match	35.4%	Score 636.4	DB 12	Length 881
Best Local Similarity	87.0%	Pred. No. 8.5e-127		
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DB				
QY	61	AGGAGACTGTGGGGACCTTTGGACCTTAGGGGGAGCCTCCACCCAAATCACGTTCTCTGCCCC	121	
DB				
QY	680	AGTTTCAGAAACCTCTGGACAAACCTCTAGGGGGTACCTTCACCTCTCTTTGAGATGTTTA	939	
DB				
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QY	1000	TAGCAACCTTGGAGGCCCTGGAGACAGAGGACTGATGSSGCACATTTCCGGAGTGCTT	1059	
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QY	1240	ATTATACCGAGCTGTTTGACACAGACATGATTGATTATGAAAGGGGGTATTTTAAA	1298	
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QY	481	ACTACGATCGAGCCGTGACACACATTTGATCGATTATGAACAGGCGGGGTTTTAAA	540	
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Search completed: October 6, 2003, 13:16:09
Job time : 2695 secs